

Scoring table:	BLOSUM62							
Gapop:	10.0 , Gapext: 0.5							
Searched:	1825181 seqs, 575374646 residues							
Total number of hits satisfying chosen parameters:	1825181							
Minimum DB seq length:	0							
Maximum DB seq length:	2000000000							
Post-processing: Minimum Match 0%								
Maximum Match 100%								
Listing first 4 summaries								
Database :	UniProt_02: 1: uniprot_sprot: 2: uniprot_trembl: *							
Pred.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.							
SUMMARIES								
Result No.	Score	Query	Match	Length	DB	ID	Description	
1	6619	100.0	1248	1	APAF_HUMAN	Q9XBDB8	amycolatops	
2	5873.5	88.7	1249	1	APAF_MOUSE	Q7NKS50	gloeoBacter	
3	5871.5	88.7	1249	1	APAF_RAT	Q7NHS82	gloeoBacter	
4	5863.5	88.6	1249	2	Q8V166	Q9ePV5	mechanosarc	
5	4054.0	61.2	1248	2	Q6GNW6	Q8v665	Q8TMS3	
6	3683.5	55.7	1261	1	APAF_BEAR_E	Q6gnu6	Q9UJ59	mechanosarc
7	1066.0	16.1	258	2	Q80VR5	Q9i948	Q8TMS3	
8	732.0	11.1	1227	1	Q8Z0R1	Q9i948	Q8TMS3	
9	728.5	11.0	1258	1	Y500_ANAS_P	Q8z0r1	anabaena sp	
10	693.0	10.5	1184	2	Q7ND85	Q8ytc2	anabaena sp	
11	691.0	10.4	1526	1	YY46_ANAS_P	Q8yxr1	gloeoBacter	
12	689.5	10.4	1197	1	Q7Nj67	Q7njk4	anabaena sp	
13	677.5	10.2	1711	2	Q8Z019	Q8yzz3	anabaena sp	
14	672.0	10.2	1683	1	YL24_ANAS_P	Q8yv57	anabaena sp	
15	666.0	10.1	1193	2	Q7ND05	Q7nd05	gloeoBacter	
16	659.0	10.0	1188	2	Q7ND80	Q7nd80	gloeoBacter	
17	643.5	9.7	1356	1	HBT1_PODAN	Q00808	podospora a	
18	626.0	9.5	1693	1	Y163_SKNY3	Q55563	synchocyst	
19	624.5	9.4	1356	2	Q8X1P4	Q8x1p4	podospora a	
20	614.5	9.3	934	2	Q8YZ23	Q8yz23	anabaena sp	
21	611.5	9.2	1551	2	Q8YMU3	Q8ymu3	anabaena sp	
22	610.0	9.2	1708	2	Q8YZ12	Q8yz12	anabaena sp	
23	609.0	9.2	1081	2	Q7NCCT8	Q7ncct8	gloeoBacter	
24	606.5	9.2	1356	2	Q8X1P3	Q8x1p3	podospora a	
25	605.5	9.1	1356	2	Q8X1P5	Q8x1p5	podospora a	
26	604.5	9.1	1376	2	Q8X1P2	Q8x1p2	anabaena sp	
27	600.5	9.1	1189	2	Q8YL09	Q8yl09	anabaena sp	
28	586.0	8.9	1183	2	Q7NL89	Q7nl89	gloeoBacter	
29	581.0	8.8	1233	2	Q8TMX4	Q8tmx4	methanosa	
30	580.5	8.8	1189	2	Q8YTD1	Q8ytd1	anabaena sp	
31	561.5	8.5	1747	2	Q8Z020	Q8z020	anabaena sp	

ALIGNMENTS

RESULT 1	
APAF_HUMAN	STANDARD; PRT; 1248 AA.
ID	APAF_HUMAN
AC	O14777; Q43297; Q74438; Q9BX26; Q9UB25; Q9UGN9; Q9UGP0; Q9UJ58; Q9UJ59; Q9UJ60; Q9UJ62; Q9UJ63; Q9UJ64; Q9UJ65;
AC	Q9UJ66; Q9UJ67; Q9UNC9;
AC	Q9UJ68; Q9UJ69; Q9UJ70; Q9UJ71; Q9UJ72; Q9UJ73; Q9UJ74; Q9UJ75;
DT	15-JUL-1998 (Rel. 36, Created)
DT	28-FEB-2003 (Rel. 41, Last sequence update)
DT	01-OCT-2004 (Rel. 45, Last annotation update)
DE	Apoptotic protease activating factor 1 (Apaf-1).
GN	Name=APAF1; Synonyms=KIAA0413;
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo. Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1] _TaxID=9606;
RP	SEQUENCE FROM N.A. (ISOFORM 3), AND PARTIAL SEQUENCE.
RC	SEQUENCE FROM N.A. (ISOFORM 3), AND PARTIAL SEQUENCE.
RX	TISSUE=Cervical carcinoma; MEDLINE=97410306; PubMed=9267021;
RA	Zou H., Henzel W.J., Liu X., Lutborg A., Wang X.; "Apaf-1, a human protein homologous to C. elegans CED-4, participates in cytochrome c-dependent activation of caspase-3." Cell 90:405-413 (1997).
RT	RT
RL	RT
RN	[2]
RP	SEQUENCE FROM N.A. (ISOFORMS 1, 4 AND 5).
RC	SEQUENCE FROM N.A. (ISOFORMS 1, 4 AND 5). TISSUE=T-cell; MEDLINE=93292265; PubMed=10364241;
RC	SEQUENCE FROM N.A. (ISOFORMS 1, 4 AND 5). TISSUE=Cervical carcinoma, Heart, and Peripheral blood; MEDLINE=98373149; PubMed=101414947; DOI:10.1006/birc.1999.1124;
RX	Rahn C., Hirsch B., Juhue D., Duerkop H., Stein H.; "Three new types of Apaf-1 in mammalian cells." Biochem. Biophys. Res. Commun. 261:746-749 (1999).
RA	"Three new types of Apaf-1 in mammalian cells." Biochem. Biophys. Res. Commun. 274:1794-1795 (1999).
RT	RT
RL	RL
RN	[3]
RP	SEQUENCE FROM N.A. (ISOFORM 2).
RC	SEQUENCE FROM N.A. (ISOFORM 2).
RX	Rahn C., Hirsch B., Juhue D., Duerkop H., Stein H.; "Three new types of Apaf-1 in mammalian cells." Biochem. Biophys. Res. Commun. 274:1794-1795 (1999).
RA	"Three new types of Apaf-1 in mammalian cells." Biochem. Biophys. Res. Commun. 261:746-749 (1999).
RT	RT
RL	RL
RN	[4]
RP	SEQUENCE FROM N.A. (ISOFORM 1), FUNCTION, SUBUNITS, AND MUTAGENESIS OF LYS-160 AND MET-368.
RC	SEQUENCE FROM N.A. (ISOFORM 1), FUNCTION, SUBUNITS, AND MUTAGENESIS OF LYS-160 AND MET-368.
RX	MEDLINE=9332175; PubMed=10393175;
RA	Saleh A., Srinivasula S.M., Acharya S., Fishel R., Alnemri E.S.; "Cytochrome c and dATP/ATP hydrolysis in Apaf-1-mediated oligomerization of Apaf-1 is a prerequisite for procaspase-9 activation." J. Biol. Chem. 274:1794-1795 (1999).
RT	RT
RT	RT
RL	RL
RN	[5]
RP	SEQUENCE FROM N.A. (ISOFORM 2).
RA	Ohara O.; Submitted (MAY-2002) to the EMBL/GenBank/DDJB databases.
RN	[6]
RP	SEQUENCE OF 355-1248 FROM N.A. (ISOFORM 2).
RC	TISSUE=Brain;

RX MEDLINE=98116655; PubMed=9455477; Name=3; Synonyms=Apaf-1S;
 RA Ishikawa K.-I., Nagae T., Nakajima D., Seki N., Ohira M., IsoID=O141227-3; Sequence=VSP_006759;
 RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; Name=4; Synonyms=Apaf-1M;
 RT "Prediction of the coding sequences of unidentified human genes. VIII. IsoID=O141227-4; Sequence=VSP_006761;
 RT 78 new cDNA clones from brain which code for large proteins in IsoID=O141227-5; Sequence=VSP_006760; VSP_006761, VSP_006762;
 RT vitro." IsoID=O141227-6; Sequence=VSP_006761, VSP_006762;
 RN 4:307-313 (1997). IsoID=O141227-7; Sequence=VSP_008965, VSP_008966;
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 6), FUNCTION, AND SUBCELLULAR LOCATION. IsoID=O141227-8; Sequence=VSP_008966;
 RC TISSUE-Prostatic carcinoma; IsoID=O141227-9; Sequence=VSP_008966;
 RX MEDLINE=22689499; PubMed=12804598; DOI=10.1016/S0006-291X(03)00995-1; IsoID=O141227-10; Sequence=VSP_008966;
 RA Ogawa T., Shiga K., Habimoozo S., Kobayashi T., Horii A., Furukawa T.; IsoID=O141227-11; Sequence=VSP_008966;
 RT "Apaf-1-Alt," a novel alternative splicing form of Apaf-1, potentially causes impaired undergoing DNA damage-induced apoptosis in IsoID=O141227-12; Sequence=VSP_008966;
 RT the LNCAP human prostate cancer cell line." IsoID=O141227-13; Sequence=VSP_008966;
 RL Biochem. Biophys. Res. Commun. 306:537-543 (2003). IsoID=O141227-14; Sequence=VSP_008966;
 RN IsoID=O141227-15; Sequence=VSP_008966;
 RP SEQUENCE OF 810-864 AND 866-883 FROM N.A. IsoID=O141227-16; Sequence=VSP_008966;
 RA Roberts D.L., Dalgleish R., Cohen G.M., MacFarlane M.; IsoID=O141227-17; Sequence=VSP_008966;
 RT "The mammalian CED4 homologue, Apaf1, exists as two distinct forms in IsoID=O141227-18; Sequence=VSP_008966;
 RT human cells"; IsoID=O141227-19; Sequence=VSP_008966;
 RL submitted (MAR-1999) to the EMBL/GenBank/DBJ databases. IsoID=O141227-20; Sequence=VSP_008966;
 RN IsoID=O141227-21; Sequence=VSP_008966;
 RP SEQUENCE OF 1-138 FROM N.A. (ISOFORM 1/4/5). IsoID=O141227-22; Sequence=VSP_008966;
 RA Won M., Lee J.-W., Ohr H.-H., Kim D.-U., Chung K.-S., Lee M.; IsoID=O141227-23; Sequence=VSP_008966;
 RA Yoo H.-S.; IsoID=O141227-24; Sequence=VSP_008966;
 RT "Cloning of variant Apaf1", Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases. IsoID=O141227-25; Sequence=VSP_008966;
 RN IsoID=O141227-26; Sequence=VSP_008966;
 RP APAF-1-MEDIATED OLIGOMERIZATION. IsoID=O141227-27; Sequence=VSP_008966;
 RX MEDLINE=98115378; PubMed=96511578; IsoID=O141227-28; Sequence=VSP_008966;
 RA Moroni M.C., Hickman E.S., Denchi E.L., Caprara G., Colli E.; IsoID=O141227-29; Sequence=VSP_008966;
 RA Cecconi F., Mueller H., Heijnen K.; IsoID=O141227-30; Sequence=VSP_008966;
 RA "Apaf-1 is a transcriptional target for B2F and p53." IsoID=O141227-31; Sequence=VSP_008966;
 RT Mol. Cell Biol. 3:552-558 (2001). IsoID=O141227-32; Sequence=VSP_008966;
 RL IsoID=O141227-33; Sequence=VSP_008966;
 RP INDUCTION BY E2F AND P53. IsoID=O141227-34; Sequence=VSP_008966;
 RX MEDLINE=21283226; PubMed=11389439; DOI=10.1038/35078527; IsoID=O141227-35; Sequence=VSP_008966;
 RA Moroni M.C., Hickman E.S., Denchi E.L., Caprara G., Colli E.; IsoID=O141227-36; Sequence=VSP_008966;
 RA Cecconi F., Mueller H., Heijnen K.; IsoID=O141227-37; Sequence=VSP_008966;
 RA "Apaf-1 is a transcriptional target for B2F and p53." IsoID=O141227-38; Sequence=VSP_008966;
 RT Mol. Cell Biol. 3:552-558 (2001). IsoID=O141227-39; Sequence=VSP_008966;
 RL IsoID=O141227-40; Sequence=VSP_008966;
 RP X-RAY CRYSTALLOGRAPHY (1.3 ANGSTROMS). OF 1-97. IsoID=O141227-41; Sequence=VSP_008966;
 RX MEDLINE=220013099; PubMed=10541391; DOI=10.1006/jmbi.1999.3177; IsoID=O141227-42; Sequence=VSP_008966;
 RA Vaughn D.E., Rodriguez J., Lazebnik Y.; IsoID=O141227-43; Sequence=VSP_008966;
 RA "Crystal structure of Apaf-1 caspase recruitment domain: an alpha-helical key fold for apoptotic signaling." IsoID=O141227-44; Sequence=VSP_008966;
 RT Mol. Biol. 293:339-447 (1998). IsoID=O141227-45; Sequence=VSP_008966;
 RL IsoID=O141227-46; Sequence=VSP_008966;
 RP STRUCTURE BY NMR OF 1-97. IsoID=O141227-47; Sequence=VSP_008966;
 RX MEDLINE=20047184; PubMed=10578182; IsoID=O141227-48; Sequence=VSP_008966;
 RA Day C.L., Dupont C., Lackmann M., Vaux D.L., Hinds M.G.; IsoID=O141227-49; Sequence=VSP_008966;
 RT "Solution structure and mutagenesis of the caspase recruitment domain (CARD) from Apaf-1." IsoID=O141227-50; Sequence=VSP_008966;
 RT (CARD) from Apaf-1." IsoID=O141227-51; Sequence=VSP_008966;
 RT "Cell Death Differ. 6:1125-1132 (1999)." IsoID=O141227-52; Sequence=VSP_008966;
 CC -1- FUNCTION: Oligomeric Apaf-1 mediates the cytochrome c-dependent activation of pro-caspase-9 (Apaf-1), leading to the activation of caspase-3 and apoptosis. This activation requires ATP. Isoform 6 is less effective in inducing apoptosis. IsoID=O141227-53; Sequence=VSP_008966;
 CC -1- SUBUNIT: Monomer. Oligomerizes upon binding of cytochrome c and dATP. Oligomeric Apaf-1 and pro-caspase-9 bind to each other via their respective NH2-terminal CARD domains and consecutively mature caspase-9 is released from the complex. Pro-caspase-3 is recruited into the Apaf-1-pro-caspase-9 complex via interaction with pro-caspase-9. IsoID=O141227-54; Sequence=VSP_008966;
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic. IsoID=O141227-55; Sequence=VSP_008966;
 CC Event=Alternative splicing; Named isoforms=6; IsoID=O141227-56; Sequence=VSP_008966;
 CC Name=1; Synonyms=Apaf-1XL; IsoID=O141227-57; Sequence=Displayed; IsoID=O141227-58; Sequence=Displayed; IsoID=O141227-59; Sequence=VSP_006759;
 CC IsoID=O141227-60; Sequence=VSP_006759;

CC Name=3; Synonyms=Apaf-1S; IsoID=O141227-3; Sequence=VSP_006759; VSP_006761; IsoID=O141227-4; Sequence=VSP_006761; IsoID=O141227-5; Sequence=VSP_006760; VSP_006761, VSP_006762; IsoID=O141227-6; Sequence=VSP_008965, VSP_008966; IsoID=O141227-7; Sequence=VSP_008966; IsoID=O141227-8; Sequence=VSP_008966; IsoID=O141227-9; Sequence=VSP_008966; IsoID=O141227-10; Sequence=VSP_008966; IsoID=O141227-11; Sequence=VSP_008966; IsoID=O141227-12; Sequence=VSP_008966; IsoID=O141227-13; Sequence=VSP_008966; IsoID=O141227-14; Sequence=VSP_008966; IsoID=O141227-15; Sequence=VSP_008966; IsoID=O141227-16; Sequence=VSP_008966; IsoID=O141227-17; Sequence=VSP_008966; IsoID=O141227-18; Sequence=VSP_008966; IsoID=O141227-19; Sequence=VSP_008966; IsoID=O141227-20; Sequence=VSP_008966; IsoID=O141227-21; Sequence=VSP_008966; IsoID=O141227-22; Sequence=VSP_008966; IsoID=O141227-23; Sequence=VSP_008966; IsoID=O141227-24; Sequence=VSP_008966; IsoID=O141227-25; Sequence=VSP_008966; IsoID=O141227-26; Sequence=VSP_008966; 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KW 3D-structure; Alternative splicing; Apoptosis; ATP-binding;	Db 961 EAQVSCCCLSPHQYIAFGDENGAIILELYNNRIFQSRFQHKKTVWHIQFTADEKTLIS 1020
KW Direct protein sequencing; Repeat; WD repeat.	Db 1021 SSDAIIQWNWQLDKCIFLRGHOETVKDFRLLKNSRLSMSFDGTVKWNLITCNKEKD 1080
Query Match 100.0%; Score 6619; DB 1; Length 1248;	Qy 1021 SSDAIIQWNWQLDKCIFLRGHOETVKDFRLLKNSRLSMSFDGTVKWNLITCNKEKD 1080
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;	Db 1021 SSDAIIQWNWQLDKCIFLRGHOETVKDFRLLKNSRLSMSFDGTVKWNLITCNKEKD 1080
Matches 1248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Qy 1081 FVCHQGTVLSDIISHATKFESTSADTAKWSFDLPLBLRGLINGCYRCSAFSVDST 1140
1 MDAKARNCLLOREALEKDIKTSYMDHMISPGFLTSEEEKVRNRPQQRAAMLIKMI 60	Db 1081 FVCHQGTVLSDIISHATKFESTSADTAKWSFDLPLBLRGLINGCYRCSAFSVDST 1140
1 MDAKARNCLLOREALEKDIKTSYMDHMISPGFLTSEEEKVRNRPQQRAAMLIKMI 60	Qy 1141 LLATGDDNGEIRIWNYSNGELLHLCAPLSEEGAATHGGWWTDLCLFSPDGKMLISAGGYIK 1200
61 LKKDNDSYVSFYNALHEGYKDLAALIHGDIPVWSSSSGKDSVSGTTSYRTVLCBGGVP 120	Db 1141 LLATGDDNGEIRIWNYSNGELLHLCAPLSEEGAATHGGWWTDLCLFSPDGKMLISAGGYIK 1200
61 LKKDNDSYVSFYNALHEGYKDLAALIHGDIPVWSSSSGKDSVSGTTSYRTVLCBGGVP 120	Qy 1201 WNNVTGESSOTPYTNTNLKKIHYSPDFTKTYTDNLGLYLQLQLE 1248
121 QRPVVFTTRKLVNAQQLSKLKGEGWWTIGMAGCGRSVLAABARDVDSLBBCCFPG 180	Db 1201 WNNVTGESSOTPYTNTNLKKIHYSPDFTKTYTDNLGLYLQLQLE 1248
121 QRPVVFTTRKLVNAQQLSKLKGEGWWTIGMAGCGRSVLAABARDVDSLBBCCFPG 180	Qy 181 GYHWVSYGKDKGSGLIMKLQLNCLTRLDQDEFSQRQLPLNTEAKDPLRILMLRKHPRSLI 240
Db 181 GHVHWVSYGKDKGSGLIMKLQLNCLTRLDQDEFSQRQLPLNTEAKDPLRILMLRKHPRSLI 240	RESULT 2 APAF_MOUSE ID APAF_MOUSE STANDARD; PRT; 1249 AA.
Qy 241 ILDDVNDSWLKAFAKDSQCQLLTTRDKSVDTSVMGPKYVNPYESSLGKECLEILSLFVN 300	AC 088875; DT 28-FEB-2003 (Rel. 41, Created)
Db 241 ILDDVNDSWLKAFAKDSQCQLLTTRDKSVDTSVMGPKYVNPYESSLGKECLEILSLFVN 300	DT 28-FEB-2003 (Rel. 41, Last sequence update)
Db 301 MKKADLPEQANSIIKECKSPLYVLSLIGALLDRDPNRWEYTLKOLONKQFRKRKSSYD 360	DT 05-JUL-2004 (Rel. 44, Last annotation update)
Qy 301 MKKADLPEQANSIIKECKSPLYVLSLIGALLDRDPNRWEYTLKOLONKQFRKRKSSYD 360	DE Apoptotic protease activating factor 1 (Apaf-1).
Db 361 YEALDEAMSISVEMRLREDIKQYYTDTSLIQLQDMEETEYEDLILQEYFN 420	GN Name=Apaf1; OS Mus musculus (Mouse); OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. OX NCBI_TaxID=10030; [1]
Db 361 YEALDEAMSISVEMRLREDIKQYYTDTSLIQLQDMEETEYEDLILQEYFN 420	RN RP STRAIN FROM N.A. (ISOFORM 1). RN RC STRAIN-Swiss Webster/NIH Swiss; TISSUE=Embryo; RN RX MEDLINE=96424242; PubMed=9753220; RN RA Cecconi F., Alvarez-Bolado G., Meyer B.I., Roth K.A., Gruss P.; RN RT "Apaf1 (CARD-4 homolog) regulates programmed cell death in mammalian development." Cell 94:727-737(1998). RN [2]
Db 421 KSSLFCDRNGSFYRYLHDLOYDFLKEKNCSSQDLHKKITTOQYHQPTLSPQEDC 480	RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
Qy 421 KSSLFCDRNGSFYRYLHDLOYDFLKEKNCSSQDLHKKITTOQYHQPTLSPQEDC 480	RC TISSUE=Spleen; MEDLINE=21063441; PubMed=11119689; DOI=10.1016/S0006-8993(00)02916-4; RC RA Walker D.W., Morgan J.T.; RA "A comparison of the expression and properties of Apaf-1 and Apaf-1L." Brain Res. 886:73-81(2000).
Db 421 KSSLFCDRNGSFYRYLHDLOYDFLKEKNCSSQDLHKKITTOQYHQPTLSPQEDC 480	RT -1- SUBUNIT: Monomer. Oligomeric Apaf-1 mediates the cytochrome c-dependent activation of pro-caspase-9 bind to each other via their respective NH2-terminal CARD domains and consecutively mature caspase-9 is released from the complex (By similarity). It may also interact with Bcl-XL. RT -1- SUBCELLULAR LOCATION: Cyctoplasmic (By similarity).
Qy 481 MYWNFLAYMASAOKHKELKALMFSDWIKAKTLYGVPAHLIHEVYRHLDEDCAV 540	CC -1- FUNCTION: Oligomeric Apaf-1 mediates the cytochrome c-dependent activation of pro-caspase-9 (Apaf-3), leading to the activation of caspase-3 and apoptosis. This activation requires ATP (By similarity).
Db 481 MYWNFLAYMASAOKHKELKALMFSDWIKAKTLYGVPAHLIHEVYRHLDEDCAV 540	CC -1- SUBUNIT: Monomer. Oligomeric Apaf-1 and pro-caspase-9 bind to each other via their respective NH2-terminal CARD domains and consecutively mature caspase-9 is released from the complex (By similarity). It may also interact with Bcl-XL. CC -1- ALTERNATIVE PRODUCTS: CC Event-Alternative splicing; Named isoforms=2; CC Name=Apaf1L; CC IsoId=088879-1; Sequence=Displayed; CC Note=Major isoform; Name=Apaf1;
Qy 541 SENFORPSLNGHLLGRQPFNPVOLQGLCEPETSEYQOAKLQAOBVNDGMYLEWINK 600	CC IsoId=088879-2; Sequence=VSP_006763;
Db 541 SENFORPSLNGHLLGRQPFNPVOLQGLCEPETSEYQOAKLQAOBVNDGMYLEWINK 600	CC -1- TISSUE SPECIFICITY: Highly expressed in lung and spleen, weakly in brain and kidney and not detectable in liver.
Db 601 KNITNLRSLVYRPTDAHFSEQRASGADKTLYQVKAETGEKLEIKAHEDEV 660	CC -1- DEVELOPMENTAL STAGE: High levels in embryonic brain and liver from E11.5 to E17.5 day.
Qy 601 KNITNLRSLVYRPTDAHFSEQRASGADKTLYQVKAETGEKLEIKAHEDEV 660	CC -1- SIMILARITY: Contains 1 CARD domain.
Db 601 KNITNLRSLVYRPTDAHFSEQRASGADKTLYQVKAETGEKLEIKAHEDEV 660	CC -1- SIMILARITY: Contains 1 NB-ARC domain.
Db 721 SDCFLKLWDLNQKECERNMFGHTNSYNHCRFSPDDKLASCASDGTKLWDATSAKERKS 780	CC -1- SIMILARITY: Contains 13 WD repeats.
Qy 721 SDCFLKLWDLNQKECERNMFGHTNSYNHCRFSPDDKLASCASDGTKLWDATSAKERKS 780	CC
Db 721 SDCFLKLWDLNQKECERNMFGHTNSYNHCRFSPDDKLASCASDGTKLWDATSAKERKS 780	CC
Qy 781 INVKQFLNLDPQDEMIVTKCCSMYSDGARIMVAKNKFLFDIHTSGLGEIHTGH 840	CC
Db 781 INVKQFLNLDPQDEMIVTKCCSMYSDGARIMVAKNKFLFDIHTSGLGEIHTGH 840	CC
Qy 841 STIQYCDSPQHLLAVALSQCVELWNTDERSKVADRGHLSWTHGVMFSPDGSSFLTS 900	CC
Db 841 STIQYCDSPQHLLAVALSQCVELWNTDERSKVADRGHLSWTHGVMFSPDGSSFLTS 900	CC
Qy 901 SDDQTIRLWETKVKKNISAVMLQKEVDVQFQNENMVLADHIRRLQLINGRTQDYLTT 960	CC
Db 901 SDDQTIRLWETKVKKNISAVMLQKEVDVQFQNENMVLADHIRRLQLINGRTQDYLTT 960	CC
Qy 961 EAQVSCCCLSPHQYIAFGDENGAIILELYNNRIFQSRFQHKKTVWHIQFTADEKTLIS 1020	CC

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 or send an email to license@isb-sib.ch).

DR EMBL; AF064071; AA626458.1; - .

DR HSSP; Q9Y291; 1P22.

DR MGD; MG1:1;06796; Apaf1.

DR GO; GO:0007420; P:apoptotic protease activator activity; IPI.

DR GO; GO:0007420; P:brain development; IMP.

DR GO; GO:0007275; P:development; IMP.

DR InterPro; IPR001315; CARD.

DR InterPro; IPR01029; DEATH like.

DR InterPro; IPR003182; NB-ARC.

DR InterPro; IPR01680; WD40.

DR InterPro; IPR011046; WD40_like.

DR Pfam; PF00619; CARD_1.

DR Pfam; PF000831; NB-ARC_1.

DR Pfam; PF00400; WD40_13.

DR PRINTS; PRO0320; PROTEINBRDT.

DR ProDom; PD00018; WD40; 3 .

DR SMART; SM00320; WD40; 13 .

DR PROSITE; PS50209; CARD_1.

DR PROSITE; PS00678; WD_REPEATS_1; 4 .

DR PROSITE; PS50083; WD_REPEATS_2; 9 .

DR PROSITE; PS00294; WD_REPEATS_REGION_1; Repeat; WD repeat.

KW Alternative splicing; Apoptosis; ATP-binding; Repeat; WD repeat.

FT DOMAIN 1 90 CARD.

FT DOMAIN 106 415 NB-ARC.

FT NP_BIND 154 161 ATP (Potential) .

FT REPEAT 655 694 WD 1.

FT REPEAT 655 694 WD 2.

FT REPEAT 655 738 WD 3.

FT REPEAT 741 780 WD 4.

FT REPEAT 796 837 WD 5.

FT REPEAT 838 877 WD 6.

FT REPEAT 880 919 WD 7.

FT REPEAT 959 998 WD 8.

FT REPEAT 1001 1040 WD 9.

FT REPEAT 1042 1080 WD 10.

FT REPEAT 1083 1122 WD 11.

FT REPEAT 1125 1164 WD 12.

FT REPEAT 1176 1213 WD 13.

FT VARSPLIC 99 110 GRDGGTTSFV -> A (in isoform 2) .

FT SEQNEC 1249 AA; 140888 MW; 53D91E59CE6025C CREG64;

Query Match 88.7%; Score 5873.5%; DB 1; Length 1249;

Best Local Similarity 87.5%; Prod. No. 0; Gaps 1;

Matches 1093; Conservative 79; Mismatches 76; Indels 1;

Qy 1 MDAKARNCLHREALEDKITSYIMDIMISGFLTISREBEKVRNEPQQQAAALIRMI 60

Db 1 MDAKARNCLHREALEDKITSYIMDIMISGFLTISREBEKVRNEPQQQAAALIRMI 60

Qy 61 LKDDNDSYVSYNALLHEGYKDIAALLHDGIPVYSSSGKDVSYGITSYVRVTCRGGV 120

Db 61 LKDDNDSYVSYNALLHEGYKDIAALLHDGIPVYSSSGKDVSYGITSYVRVTCRGGV 120

Qy 121 QREVFYTRKLVNAIQQKLSKLKGEPWVTHGMAGCCSKVLAEAATRDHSILEGCFFG 180

Db 121 QREVFYTRKLVNAIQQKLSKLKGEPWVTHGMAGCCSKVLAEAATRDHSILEGCFFG 180

Qy 181 GHWWVSYVKQDQSGLMKLNLCRLDDEFSQRPLNTEAKDRGLTLMRGRHRSLL 240

Db 181 GHWWVSYVKQDQSGLMKLNLCRLDDEFSQRPLNTEAKDRGLTLMRGRHRSLL 240

Qy 241 ILDDWDWSWVLUKAEDSQCQLLTTRDKSYTDSVGMGPXKTYPVESLIGKEKGELLSLFVN 300

Db 241 ILDDWDWSWVLUKAEDSQCQLLTTRDKSYTDSVGMGPXKTYPVESLIGKEKGELLSLFVN 300

RESULT 3
 APAF RAT ID APAF RAT
 STANDARD; ID APAF RAT
 Q9EP75; AC DT
 28-Feb-2003 (Rel. 41, Created)
 28-Feb-2003 (Rel. 41, Last sequence update)
 05-Jul-2004 (Rel. 44, Last annotation update)

PRT; 1249 AA.
 STANDARD;
 ID APAF RAT
 DT
 AC

KWNNVVTGEBSOFTYINGTNILKKCHVSPDFKTTVTVNLGLYLLOTLE 1248
 KWNVATEDSOTFYINGTNILKKCHVSPDFRTVTVNLGLYLQVLB 1249

PRT; 1249 AA.
 STANDARD;
 ID APAF RAT
 DT
 AC

KWNNVVTGEBSOFTYINGTNILKKCHVSPDFKTTVTVNLGLYLLOTLE 1248
 KWNVATEDSOTFYINGTNILKKCHVSPDFRTVTVNLGLYLQVLB 1249

DB	Apoptotic protease activating factor 1 (Apaf-1).		FT	REPEAT	880	919	WD 7.
GN	Name=apaf1;		FT	REPEAT	959	998	WD 8.
OS	Rattus norvegicus (Rat).		FT	REPEAT	1001	1040	WD 9.
OC	Bukarota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		FT	REPEAT	1042	1080	WD 10.
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		FT	REPEAT	1083	1122	WD 11.
NCBI_TaxID=10116;			FT	REPEAT	1125	1164	WD 12.
OX			FT	REPEAT	1176	1213	WD 13.
RN	{1}		SQ	SEQUENCE	1249	AA:	141151 MW: 7B4A8116FAD008E9 CRC54;
RP	SEQUENCE FROM N.A.						
RC	STRAIN=Sprague-Dawley;						
RA	Itoh T., Itoh A., Pleasure D.;						
RL	Submitted (NOV-2000) to the ENBL/GenBank/DDBJ databases.						
RN	[2]						
RP	DEVELOPMENTAL REGULATION, AND INDUCTION BY BRAIN INJURY.						
RX	MEDLINB=21450943; PubMed=1567033;						
RA	Yakovlev A.G., Ota K., Wang G., Movsesyan V., Bao W.-L., Yoshihara K.,						
RA	Faden A.I.;	"Differential expression of apoptotic protease-activating factor-1 and caspase-3 genes and susceptibility to apoptosis during brain development and after traumatic brain injury.";					
RL	J. Neurosci. 21:7439-7446 (2001).						
CC	-!- FUNCTION: Regulates programmed cell death; necessary for normal brain development. Participates with caspase-9 (Apaf-3) in the cytochrome c-dependent activation of caspase-3, leading to apoptosis. This activation requires ATP (By similarity). -!-		CC	CC	1 MDAKARNCLIQHREALEKDIKTYSYIMDHMISDGFITISEBEKVRNEPTOCQRAAMLIKMI 60		
CC	CC	RT	LNKKNDISYVSYNNALIHEGYKDALLHGIPVQVSSGKDSVGSGTTSYRTVLCGGVP 120		1 MDAKARNCLIQHKEALEKDIKTYSYIMDHMISNGVITVEEKVKSGATQYORAAALIKMI 60		
CC	CC	RT	61 LNKKNDISYVSYNNALIHEGYKDALLHGIPVQVSSGKDSVGSGTTSYRTVLCGGVP 120		61 LNKKNDISYVSYNNALIHEGYKDALLHGIPVQVSSGKDSVGSGTTSYRTVLCGGVP 120		
CC	CC	RT	61 LNKKNDISYVSYNNALIHEGYKDALLHGIPVQVSSGKDSVGSGTTSYRTVLCGGVP 120		61 LNKKNDISYVSYNNALIHEGYKDALLHGIPVQVSSGKDSVGSGTTSYRTVLCGGVP 120		
CC	CC	CC	CC	CC	121 QRPVVFVTRKLVLNAQQLSKLKGSPGVWTHGAGCGSIVLAEAARDISLLBCFCFG 180		
CC	CC	CC	CC	CC	121 QRPVVFVTRKLVLNAQQLSKLKGSPGVWTHGAGCGSIVLAEAARDISLLBCFCFG 180		
CC	CC	CC	CC	CC	121 QRPVVFVTRKLVLNAQQLSKLKGSPGVWTHGAGCGSIVLAEAARDISLLBCFCFG 180		
CC	CC	CC	CC	CC	181 GHWWSIGKDKGIGLMLKLONLCTPLDQDESFSQSPLNTEAKDLRILMKRKPSSL 240		
CC	CC	CC	CC	CC	181 GHWWSIGKDKGIGLMLKLONLCTPLDQDESFSQSPLNTEAKDLRILMKRKPSSL 240		
CC	CC	CC	CC	CC	181 GHWWSIGKDKGIGLMLKLONLCTPLDQDESFSQSPLNTEAKDLRILMKRKPSSL 240		
CC	CC	CC	CC	CC	181 GHWWSIGKDKGIGLMLKLONLCTPLDQDESFSQSPLNTEAKDLRILMKRKPSSL 240		
CC	CC	CC	CC	CC	241 ILDDWDWSYLKAFLPSQCCQILLTFRDKSVDTSVCPKTVPPVSESSLGKEGLEISLFLVN 300		
CC	CC	CC	CC	CC	241 ILDDWDWSYLKAFLPSQCCQILLTFRDKSVDTSVCPKTVPPVSESSLGKEGLEISLFLVN 300		
CC	CC	CC	CC	CC	241 ILDDWDWSYLKAFLPSQCCQILLTFRDKSVDTSVCPKTVPPVSESSLGKEGLEISLFLVN 300		
CC	CC	CC	CC	CC	301 MKKADIPQEHSIIKECKGSPLWLSLGLLARDPFRNWEYLQDQNLQFRIRKSSSYD 360		
CC	CC	CC	CC	CC	301 MKKEDIPVEHSIIKECKGSPLWLSLGLLARDPFRNWEYLQDQNLQFRIRKSSSYD 360		
CC	CC	CC	CC	CC	361 YEALDEAMSISVEMREDIKDYTTDLSLHQDKVYPTKVCLWDMETEEVEDLLOFVN 420		
CC	CC	CC	CC	CC	361 YEALDEAMSISVEMREDIKDYTTDLSLHQDKVYPTKVCLWDMETEEVEDLLOFVN 420		
CC	CC	CC	CC	CC	421 KSLLFCDRNGKSFRYTLHLQDFLTPEKNSQOLHKKLTITOPRYHOPTLSPQQEDC 480		
CC	CC	CC	CC	CC	421 KSLLFCDRNGKSFRYTLHLQDFLTPEKNSQOLHKKLTITOPRYHOPTLSPQQEDC 480		
CC	CC	CC	CC	CC	421 KSLLFCDRNGKSFRYTLHLQDFLTPEKNSQOLHKKLTITOPRYHOPTLSPQQEDC 480		
CC	CC	CC	CC	CC	481 MYWNPFLAYIMASAMKHKELCALMSLDWTKATEVPHYLHPEVYHILDEKDCAV 540		
CC	CC	CC	CC	CC	481 MYWNPFLAYIMASAMKHKELCALMSLDWTKATEVPHYLHPEVYHILDEKDCAV 540		
CC	CC	CC	CC	CC	601 KNITLISRLVYRPTDAVTHAQSEDQASCQADKTLYQPKATGEKLEIKAHEDEV 660		
CC	CC	CC	CC	CC	601 KNITLISRLVYRPTDAVTHAQSEDQASCQADKTLYQPKATGEKLEIKAHEDEV 660		
CC	CC	CC	CC	CC	601 KTIKNLISRLVYRPTDAVTHACRSQDQASCQADKTLYQPKATGEKLEIKAHEDEV 660		
CC	CC	CC	CC	CC	601 KTIKNLISRLVYRPTDAVTHACRSQDQASCQADKTLYQPKATGEKLEIKAHEDEV 660		
DR	HSSP; P16619; IERJ.		DR	SDCFKLWDLNQKECRNTMFGHTNVSNHCRSPDPDKLASSADGTLLKMDATSAEKRS 780			
DR	RGD; 620575; Apaf1.		DR	721 NDSFLWLQDNQKECRNTMFGHTNVSNHCRSPDPDKLASSADGTLLKMDATSAEKRS 780			
DR	InterPro; IPR011315; CARD.		DR	721 INVKEFFNLEDPOQDMEVYVKCCWSADGARIMAAKNIKIELPDIHTSGLGEHTGH 840			
DR	InterPro; IPR011029; DEATH like.		DR	721 INVKEFFNLEDPOQDMEVYVKCCWSADGARIMAAKNIKIELPDIHTSGLGEHTGH 840			
DR	InterPro; IPR002182; NB-ARC.		DR	721 INVKEFFNLEDPOQDMEVYVKCCWSADGARIMAAKNIKIELPDIHTSGLGEHTGH 840			
DR	InterPro; IPR004106; Peptidase_S9A_N.		DR	721 INVKEFFNLEDPOQDMEVYVKCCWSADGARIMAAKNIKIELPDIHTSGLGEHTGH 840			
DR	InterPro; IPR011046; WD40.		DR	721 INVKEFFNLEDPOQDMEVYVKCCWSADGARIMAAKNIKIELPDIHTSGLGEHTGH 840			
DR	InterPro; IPR011046; WD40_1-like.		DR	721 INVKEFFNLEDPOQDMEVYVKCCWSADGARIMAAKNIKIELPDIHTSGLGEHTGH 840			
PFam	Pf00931; NB-ARC.		DR	721 INVKEFFNLEDPOQDMEVYVKCCWSADGARIMAAKNIKIELPDIHTSGLGEHTGH 840			
PFam	Pf009400; WD40.		DR	721 INVKEFFNLEDPOQDMEVYVKCCWSADGARIMAAKNIKIELPDIHTSGLGEHTGH 840			
DR	PRINTS; PRO0320; GPROTEINBRPT.		DR	721 INVKEFFNLEDPOQDMEVYVKCCWSADGARIMAAKNIKIELPDIHTSGLGEHTGH 840			
DR	ProDom; PD000018; WD40; 3.		DR	721 INVKEFFNLEDPOQDMEVYVKCCWSADGARIMAAKNIKIELPDIHTSGLGEHTGH 840			
SMART	SM00320; WD40; 13.		DR	721 INVKEFFNLEDPOQDMEVYVKCCWSADGARIMAAKNIKIELPDIHTSGLGEHTGH 840			
DR	PROSITE; PS50209; CARD; 1.		DR	721 INVKEFFNLEDPOQDMEVYVKCCWSADGARIMAAKNIKIELPDIHTSGLGEHTGH 840			
DR	PROSITE; PS00678; WD_REPEATS_1; 4.		DR	721 INVKEFFNLEDPOQDMEVYVKCCWSADGARIMAAKNIKIELPDIHTSGLGEHTGH 840			
DR	PROSITE; PS50082; WD_REPEATS_2; 9.		DR	721 INVKEFFNLEDPOQDMEVYVKCCWSADGARIMAAKNIKIELPDIHTSGLGEHTGH 840			
DR	PROSITE; PS50294; WD_REPEATS_REGION; 1.		DR	721 INVKEFFNLEDPOQDMEVYVKCCWSADGARIMAAKNIKIELPDIHTSGLGEHTGH 840			
KW	Apoptosis; ATP-binding; Repeat; WD repeat.		DR	721 INVKEFFNLEDPOQDMEVYVKCCWSADGARIMAAKNIKIELPDIHTSGLGEHTGH 840			
FT	DOMAIN 1	90	CARD.	721 INVKEFFNLEDPOQDMEVYVKCCWSADGARIMAAKNIKIELPDIHTSGLGEHTGH 840			
FT	DOMAIN 106	415	NB-ARC.	721 INVKEFFNLEDPOQDMEVYVKCCWSADGARIMAAKNIKIELPDIHTSGLGEHTGH 840			
NP_BIND	154	161	ATP (Potential).	721 INVKEFFNLEDPOQDMEVYVKCCWSADGARIMAAKNIKIELPDIHTSGLGEHTGH 840			
FT	REPEAT 613	652	WD 1.	721 INVKEFFNLEDPOQDMEVYVKCCWSADGARIMAAKNIKIELPDIHTSGLGEHTGH 840			
FT	REPEAT 655	694	WD 2.	721 INVKEFFNLEDPOQDMEVYVKCCWSADGARIMAAKNIKIELPDIHTSGLGEHTGH 840			
FT	REPEAT 697	738	WD 3.	721 INVKEFFNLEDPOQDMEVYVKCCWSADGARIMAAKNIKIELPDIHTSGLGEHTGH 840			
FT	REPEAT 741	780	WD 4.	721 INVKEFFNLEDPOQDMEVYVKCCWSADGARIMAAKNIKIELPDIHTSGLGEHTGH 840			
FT	REPEAT 796	837	WD 5.	721 INVKEFFNLEDPOQDMEVYVKCCWSADGARIMAAKNIKIELPDIHTSGLGEHTGH 840			
FT	REPEAT 838	877	WD 6.	721 INVKEFFNLEDPOQDMEVYVKCCWSADGARIMAAKNIKIELPDIHTSGLGEHTGH 840			

Qy 901 SDDOTIRLWETKVKVCKNSAAMLKOEVDTYFQENEVATAYDHIRRQLINGRQGQIDYL T 960
 Db 901 SDDOTIRLWETKVKVCKNSAATVLKQIDYVFQENEMMAYLAVINIRGLLQLAGTQIYLP 960
 Qy 961 EAQVSCCCISPHLQYIAFGDENGAIEIELFLVNNRIFQSRFHDKKTMHIOFTADEKLIS 1020
 Db 961 EAQVSCCCISPHLQYIAFGDEGAIKITELPNRVRFSSGTCGHGAVRHIOFTADGKLIS 1020
 Qy 1021 SDDAEIOWWNQLDCTFRIGHQTVDFLRLKNSLLSISFDCTVKNWNTGNEKEKD 1080
 Db 1021 SSEUSVIQWNNQTEEVFLQAHQETVDFRLRDSRLSMSFDCTVKNWNTGRIERD 1080
 Qy 1081 FVCHQGTIVLSCDISHDATKESSTSADTAKTKSFDLPLHELRHNGCVRCAPSVDST 1140
 Db 1081 FVCHQGTIVLSCAISDATKESSTSADTAKTKSFDLPLHELRHNGCVRCAPSVDGI 1140
 Db 1141 LLATGDDNGEIRIWNVSNGELLHLICAPS_EGAAATHGGNTDLCSPDGKMLISAGGY 1199
 Qy 1141 LLATGDDNGEIRIWNVSNGELLHLICAPS_EISEGTATHGGNTDVCSPDRKMLVSAGGYL 1200
 Qy 1200 KWNWVTTGESESOFYTINGTNKIKHVSDFKTYVTVNDLGLYLTQTLB 1248
 Db 1201 KWNWVTTGESESOFYTINGTNKIKHVSDFKTYVTVNDLGLYLYLQVLE 1249

RESULT 4

Q8VIG6 PRELIMINARY; PRT; 1249 AA.
 ID Q8VIG6; AC Q8VIG6;
 DT 01-MAR-2002 (TREMBrel. 20, Created)
 DT 01-OCT-2003 (TREMBrel. 25, Last sequence update)
 DB Apoptotic protease activating factor-1.
 OS Rattus norvegicus (Rat).
 OC Bokaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1] SEQUENCE FROM N.A.
 RP TISSUE=cerabellum;
 RA Cao G.; Chen J.;
 RL Submitted (DDBJ=10116; EMBL=AF218388; AAC=AAI6935; 1; -).
 DR HSSP; PIG6649; IERJ.
 CO ; GO:00552; C: intracellular; IEA.
 DR GO; GO:00554; F: ATP binding; IEA.
 GO; GO:00833; P: peptidase activity; IEA.
 GO; GO:00555; F: protein binding; IEA.
 DR GO; GO:0042829; P: defense response to pathogen; IEA.
 InterPro; IPR002881; CARD_1.
 InterPro; IPR01315; CARD_1.
 InterPro; IPR000767; DEATH like.
 InterPro; IPR002182; NB-ARC_.
 InterPro; IPR001690; WD0.
 InterPro; IPR011046; WD0_1-like.
 Pfam; PF00619; CARD_1.
 DR SMART; SM00320; WD40_13.
 PROSITE; PS010209; CARD_1.
 DR PROSITE; PS00678; WD REPEATS 1; 4.
 PROSITE; PS00082; WD REPEATS 2; 9.
 DR PROSITE; PS0094; WD REPEATS REGION; 1.
 KW Protease; Repeat; WD repeat.
 SEQUENCE 1249 AA; 14169 MW; 2B1E639599A38 CRC64;

Qy 1089; Conservative; 84; Mismatches; 75; Indels; 1; Gaps; 1;
 Qy 1 MDACRNCLQHREALEKDITKTSYMDIMISGDFLTSEEKVRNEPTOCQARALTRIM 60
 Db 1 MDACRNCLQHKEALKEDITKTSYMDIMISGDFLTSEEKVRNEPTOCQARALTRIM 60
 Qy 61 LKCONDSYVSFTNALLHEGYDLAALLHGPVSSSGKDSVSGITSVTRTLCBEGVP 120
 Db 61 LNKONDYATISFTNALLHEGYDLAALLHGPVSSSGKDSVSGITSVTRTLCBEGVP 120
 Qy 121 QRPVIVTRKCLVNAQQLSKLKEPEWNTLHGAGCGSVTAAEAVRDHSLLLEGCPG 180
 Db 121 QRPVIVTRKCLVNAQQLSKLKEPEWNTLHGAGCGSVTAAEAVRDHSLLLEGCPG 180
 Qy 181 GHVIVSVGKDKSGLILMKLQNLQNLCTRLDODESFPSOI; PLNTNEAKDRLFLMLRKHPRSLL 240
 Db 181 GVHVVISQDKSGLAMKLNQNLCTRLGQESFSQRDLNTEAKDRLFLMLRKHPRSLL 240
 Qy 241 ILDDYWDWMLVRAFDSDQCQTLTRDKSVTDYSMGPKXVVPFESSLGKEKGKLELSLFLVN 300
 Db 241 ILDDYWDWMLVRAFDSDQCQTLTRDKSVTDYSMGPKXVVPFESSLGKEKGKLELSLFLVN 300
 Qy 301 MKKADLPPQASLIRECKGSPLVVSLGALLDIFPARWEYTKLQLOQKOFKRTRKSSYD 360
 Db 301 MKKADLPPQASLIRECKGSPLVVSLGALLDIFPARWEYTKLQLOQKOFKRTRKSSYD 360
 Qy 361 YEALDEAMSISVEMREDIKYDYYTDLSTLQKQVVKPFLCLNDMEVEVEDILQEFVN 420
 Db 361 YEALDEAMSISVEMREDIKYDYYTDLSTLQKQVVKPFLCLNDMEVEVEDILQEFVN 420
 Qy 421 KSLIFCDRNGKSFRYTLHDLIQDPLTEKNCSCOLDLHKKLTITOFYHOPTLSPDODC 480
 Db 421 KSLIFCDRNGKSFRYTLHDLIQDPLTEKNCSCOLDLHKKLTITOFYHOPTLSPDODC 480
 Qy 481 MYTYNFAYHMASAKHKECALMSLWDWKATELVGP AHLHBFVETRHDKDCAV 540
 Db 481 MYTYNFAYHMASAKHKECALMSLWDWKATELVGP AHLHBFVETRHDKDCAV 540
 Qy 541 SENQFELSLNCHLGRQPPNTVOLGICPEPTSETVQQLQAKOEVTDGMYLELINK 600
 Db 541 CENQFELSLNCHLGRQPPNTVOLGICPEPTSETVQQLQAKOEVTDGMYLELINK 600
 Qy 601 KNITNLRLRVYRPHDIAVTHACFEDGORIASCGADKTLQVKAETGEKLLEKAKHDEV 660
 DR 601 KTKNKLRLRVYRPHDIAVTHACFEDGORIASCGADKTLQVKAETGEKLLEKAKHDEV 660
 DR 601 LCCAFSTDRTIATCSVDKKKVTKWSMTPGELVHTDDBSBNQNCCHFTMSHHILLATGS 720
 DR 601 LCCAFSTDRTIATCSVDKKKVTKWSMTPGELVHTDDBSBNQNCCHFTMSHHILLATGS 720
 DR 661 SDQFLKLNDLQKCRENTMFHTNSVHCRFPDPDKLACSACTGLKNDATASNRKS 780
 DR 721 NDSPFLKLNDLQKCRENTMFHTNSVHCRFPDPDKLACSACTGLKNDATASNRKS 780
 DR 721 INVQKOFFUNLDPDMEVILVKCCSWMSADGARIMVAAKNIKFPIHTSGGLGEITHGHH 840
 DR 781 INVQKOFFUNLDPDMEVILVKCCSWMSADGARIMVAAKNIKFPIHTSGGLGEITHGHH 840
 DR 781 INVKRFPLSSBDPPEVIVKCCSWMSADGDIIVAKNKLDIHTSGGLGEITHGHH 840
 DR 841 STIQYCDFSPOHLLAVVALSOQCYELWNTDSRSKYADCRGHLSTWGMESPQGSSPLTS 900
 DR 841 STIQYCDFSPOHLLAVVALSOQCYELWNTDSRSKYADCRGHLSTWGMESPQGSSPLTS 900
 DR 901 SDDOTIRLWETKVKNSAAMLQEVDVVFQNEWVYLAYDHTROLLNGTGQDYL T 960
 DR 901 SDDOTIRLWETKVKNSAAMLQEVDVVFQNEWVYLAYDHTROLLNGTGQDYL T 960
 DR 961 EAQVSCCCISLHQLQYAFSDENGAIELLEVNRRFOSRFOHKTWHIQPZADEKLIS 1020
 DR 961 EAQVSCCCISLHQLQYAFSDENGAIELLEVNRRFOSRFOHKTWHIQPZADEKLIS 1020
 DR 1021 SSDDAEIQWVNWQDLCKCIPIRQHOETVYKDFRLKNSRSLWSWFDGTVKWNLTGNEKD 1080
 DR 1021 SSED5VQWVNWQDLCKCIPIRQHOETVYKDFRLKNSRSLWSWFDGTVKWNWTGIERD 1080

Qy	1081	FVCHQGTVLSCDISHDATKPSSTSADTKTAKIWSFDILLPLHLRQHNGCVRCSAFAVDST	1140	DR	PFan;	PF00619;	CARD;	1.
Db	1081	FTCHQGTVLSCAASSPTESTSADTKTAKIWSFPLSPHLKHNSCVRCASFSLDGI	1140	DR	PFan;	PF00931;	NB-ARC;	1.
Qy	1141	LILATGGDNGEIRIINVSNGELLHLICAPLS_EEGATHGWTNDLCFSPICKMLISAGGYI	1159	DR	PRINTS;	PR00324;	DISEASERIST.	
Db	1141	LILATGGDNGEIRIINVSQDQLHLICAPLSIEEGATHG3WYTDVCFSPIRKMLISAGGYI	1200	DR	Printom;	PD00018;	GPROTEINBRPT.	
Qy	1200	KWWAVVTGESSQTFTNGNPKKTHVSPDFKTYTVDNLGILYLTQLE	1248	DR	PROSITE;	PS50209;	CARD;	1.
Db	1201	KWWAVVTGESSQTFTINGNPKKTHVSPDFKTYTVDNLGILYLTQLE	1249	DR	PROSITE;	PS50078;	WD_REPEATS_1;	3.
Qy				DR	PROSITE;	PS50082;	WD_REPEATS_2;	9.
Db				DR	PROSITE;	PS50294;	WD_REPEATS_REGION;	1.
				KW	Hypothetical Protein;	Repeat;	WD repeat.	
				SQ	SEQUENCE;	1248 AA;	141574 MW;	822FCEAC4BE675D CRC64;
RESULT 5								
Q6GN06		PRELIMINARY;		DB	61.28;	Score 4054;	DB 2;	Length 1248;
ID		PRT;	1248 AA.					
AC	Q6GN06;							
DT	05-JUL-2004	(TREMBirel.	27, Created)					
DT	05-JUL-2004	(TREMBirel.	27, Last sequence update)					
DT	05-JUL-2004	(TREMBirel.	27, Last annotation update)					
DE		Hypothetical protein.						
OS	Xenopus laevis (African clawed frog).							
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							
OC	Xenopoda; Batrachia; Anura; Mesobatrachia; Pipidae;							
OC	Xenopodinae; Xenopidae;							
OX	NCBI_TaxID=8355;							
RN	[1]							
SEQUENCE FROM N.A.								
RC	SEQUENCE=Embryo;							
RX	MEDLINE=23388257;							
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,							
RA	Klaubner R.D., Collins F.S., Wagner L., Schuler G.D.,							
RA	Altshul S.F., Zeeberg B., Bustow K.W., Schaefer C.F., Bhat N.K.,							
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,							
RA	Diatchenko L., Matrusina K., Farmer A.A., Rubin G.M., Hong L.,							
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,							
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,							
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,							
RA	Bosak S.A., McIwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,							
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,							
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,							
RA	Fahie J., Heitton E., Kettman J., Madan A., Rodriguez S., Sanchez A.,							
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,							
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,							
RA	Richardson A.C., Grinwood J., Schmitz J., Myers R.M., Butterfield Y.P.,							
RA	Jones S.J., Marra M.A., Smailus D.E., Schein J.E.,							
RT	"Generation and initial analysis of more than 15,000 full-length human							
RT	and mouse cDNA sequences";							
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).							
RN	[2]							
SEQUENCE FROM N.A.								
RC	SEQUENCE=Embryo;							
RX	MEDLINE=23341132;							
RA	Klein S.-L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,							
RA	Richardson P.;							
RT	"Genetic and genomic tools for xenopus research: The NIH xenopus initiative.";							
RL	Dev. Dyn. 225:384-391 (2002).							
RP	SEQUENCE N.A.							
RC	SEQUENCE=Embryo;							
RA	Klein S., Strausberg R.; Submitted (JUN-2004) to the EMBL/GenBank/DDJB databases.							
CC	-1 - SIMILARITY: Contains 11 WD repeats.							
DR	InterPro; IPR001315; CARD.							
DR	InterPro; IPR000767; Disease_resist.							
DR	InterPro; IPR002182; NB-ARC.							
DR	InterPro; IPR011680; WD40_like.							
DR	InterPro; IPR011046; WD40_like.							

Qy	1081	FVCHQGTVLSCDISHDATKPSSTSADTKTAKIWSFDILLPLHLRQHNGCVRCSAFAVDST	1140	DR	PFan;	PF00619;	CARD;	1.
Db	1081	FTCHQGTVLSCAASSPTESTSADTKTAKIWSFPLSPHLKHNSCVRCASFSLDGI	1140	DR	PFan;	PF00931;	NB-ARC;	1.
Qy	1141	LILATGGDNGEIRIINVSNGELLHLICAPLS_EEGATHGWTNDLCFSPICKMLISAGGYI	1159	DR	PRINTS;	PR00324;	DISEASERIST.	
Db	1141	LILATGGDNGEIRIINVSQDQLHLICAPLSIEEGATHG3WYTDVCFSPIRKMLISAGGYI	1200	DR	Printom;	PD00018;	GPROTEINBRPT.	
Qy	1200	KWWAVVTGESSQTFTNGNPKKTHVSPDFKTYTVDNLGILYLTQLE	1248	DR	PROSITE;	PS50078;	WD_REPEATS_1;	3.
Db	1201	KWWAVVTGESSQTFTINGNPKKTHVSPDFKTYTVDNLGILYLTQLE	1249	DR	PROSITE;	PS50082;	WD_REPEATS_2;	9.
Qy				DR	PROSITE;	PS50294;	WD_REPEATS_REGION;	1.
Db				KW	Hypothetical Protein;	Repeat;	WD repeat.	
				SQ	SEQUENCE;	1248 AA;	141574 MW;	822FCEAC4BE675D CRC64;
Query Match								
Best Local Similarity 60.5%; Pred. No. 3e-227;								
Matches 757; Conservative 198; Mis matches 289; Indels 8; Gaps 4;								
Qy								
	1	MDAKARNCLQHREALNLERIKTSYMDHMISDGFLUTISBKEVNBPQQRAAMLIKMI	60					
	1	MDEKRSLLQNLQNTLVLDIRTAVIMDMAMISDQVTPPEEARVKQHTQVDKANFLINLI	60					
Qy								
	61	LKKDDNDSTSYFSYNALNLHEGYKDALLHDG1P1DQVSSGKSDVSQG1TYSVYRTVLCEGGPV	120					
Db								
Qy								
	61	LGKQHQAYVFSYNALNLHEGYKDALLLKSEAANAHISDSTKSSNGITSVQTVLCEGGPV	120					
Db								
Qy								
	121	QRPVYFVTFTRPLKTVKIQQSILYKUNVEQSGMVTYCMAGC5KSVLAAEVRDHSILEGCFCPG	180					
Db								
Qy								
	121	QRPVYFVTFTRPLKTVKIQQSILYKUNVEQSGMVTYCMAGC5KSVLAAEVRDHKILTECFCPG	180					
Qy								
	181	GVHWNSVGKDKPSGLMLQNLCTRLQDQESFSORPLNTEAKDRLTLMRKRPHRSLL	240					
Db								
Qy								
	181	GVHWNSVGKDKPSGLMLQNLCTRLQDQESFSORPLNTEAKDRLTLMRKRPHRSLL	240					
Qy								
	241	ILDDWDNSWYKAFSQCQTLITTRDKSYTDVSYMPKXYVPVSESSLGKEKGLETLSLFVN	300					
Db								
Qy								
	241	VLDDWDNSWYKAFSQCQTLITTRDKSYTDVSYMPKXYVPVSESSLGKEKGLETLSLFVN	300					
Qy								
	301	MKKALPDEQAHSLIKECKSPLVYSLIGALRDPSPNRWEYLKOLQNKOFKR1KSSSYD	360					
Db								
Qy								
	301	LKABELPSQAHSLIVKSVKSSPLVYSLIGALRDPSPNRWEYLKOLQNKOFKR1KSSSYD	360					
Qy								
	361	YEALDBAMS1SVEMLRREDIKYTDLISLQILODVKPTKYLCLWMDMEBEVDIQLQEFVN	420					
Db								
Qy								
	361	YEALDBAMS1SVDNLIKEDPREYNDPS1IEKDVKLPTQVCLWMDMERDVEDMNEQFVN	420					
Qy								
	481	MWNTNPLAYMASAKMHKELCALMSLDWKAKTCLVPAHLTHEFVEYRHLIDKDCAV	540					
Db								
Qy								
	481	VWYTHYLAYMAKANLHQDLCSLFLSNWLAKSSELFGTSHLIEFVQTNILDNQONAKA	540					
Qy								
	541	SENFBPLSUNGHLIGLGRQPPNIVQVGLCEPETSEVQAKLQKETQVAFKLEIKAHEDEV	600					
Db								
Qy								
	541	REHFQBFIAVNGHLIGLNPDISVQLGLQAEQDSEVQKQILQAKQEBELSGVLYWNWINK	600					
Db								
Qy								
	601	KNTITLRSUVRPHTDAYTAHCSEGDORTASCAGDTLQVAFKTEGEKLKIEKADEV	660					
Db								
Qy								
	661	LCCAFSTDDRFIATCSVDKVCKVTKWMSMTGELVHTYDEHSEQVNCHFTNSSHULLATGS	720					
Db								
Qy								
	661	LCCAFSTDDRFIATCSVDKVCKVTKWMSMTGELVHTYDEHSEQVNCHFTNSSHULLATGS	720					
Qy								
	721	SDCPFLWDLNQKEBNTMFGHTNSVHCRFSPPDKLASSADGTLLKWDATDSANERKS	780					
DR								
Qy								
	721	NDCCPFLWDLNQKEBNTMFGHTNSVHCRFSPPDKLASSADGTLLKWDATDSANERKS	780					
DR								
Qy								
	781	INVKGFFLNLEDPODMETVVKCCSWSADGARIVAAKNNKIFLFDINTGCLGHTGHGHH	840					
DR								
Qy								
	781	InterPro; IPR000767; Disease_resist.						
DR								
Qy								
	781	InterPro; IPR002182; NB-ARC.						
DR								
Qy								
	781	InterPro; IPR011680; WD40_like.						
DR								
Qy								
	781	InterPro; IPR011046; WD40_like.						

Qy 841 STIQCDSQNHLAVVALQYCVBLANTDSSISKVDRCRGLSMWVHGMSPGSPLTS 900
 Db 839 -ILYCDFTCINQIALASHYYVQLNDISSTKIADENAHLSWVHCKFSKSSSFLTS 896
 Qy 901 SDQQTILWEKKVKNSAMMLKOEVDVVFQNEVMVLAVDHIRRLQLINGTQGDYLT 960
 Db 897 SDQQTILWEWSNVSKPSATNLKREFDVSFNGEETVLVLTAKSDCQTLINGTGETUSO 956
 Qy 961 EAQ--YSCCCSLPHQYIAFGDENGATEILELVLNNRIFQSFRQHKCTVWHIQTDADEKT 1017
 Db 957 NTODKCVTCCLTNDYQLAIGRDGKVTDVSREBILCQLDGSATVQHCOFTADGKH 1016
 Qy 1018 LISSDDAEIOWNWYOLDKICLFRHQHTEVKDFRLKNSRLSNSFDGTWKWNITGNK 1077
 Db 1017 LVSSSDSTIRWLSLASGELELRGHKSPVFKLQESQFSFSGTVKWDLSTGKL 1076
 Qy 1078 EKDFVCHQGTYLSCDISHDATKFESTSADKTAKINSFLUPLHBRHGNGCYRCFAFSV 1137
 Db 1077 RKEFICHSETVSPDSTKESTASADKSAKINSLDSTLHELNQHOSCVRCRCFSW 1136
 Qy 1136 DSYLLAQGDNGDIBKRWNTNGELLHCAPISEBGA-ATFGGWHTDLCPSPGRMLISAG 1196
 Db 1137 DNXYLTDGDNKGKIMIWNGELKQCCDISVNNENSLIDGWYDLEFSPKSLVSSG 1196
 Qy 1197 GYTKWNNVATYGBESSOTFYINGTNLKKTHVSPDFKTYTVNDNLGLYLQTLN 1248
 Db 1197 ANKRYWDDGACKQFYTGTGNKSHLCLPFRTEVNLGLYVNLKLN 1248
 RESULT 6
 APAP_BRAVE
 ID APAP_BRAVE STANDARD PRT; 1261 AA.
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 05-JUL-2004 (Rel. 41, Last sequence update)
 DE Apoptotic protease activating factor 1 (Apaf-1).
 Name=apaf1;
 Brachyandrius rerio (Zebrafish) (Danio rerio).
 Metaxoa: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopercygii: Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 Cyprinidae; Danio.
 NCBI_TAXID=1955;
 OX [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE-20373792; PubMed=10917738;
 RI Zebrafish.; Cell Death Differ. 7:509-510 (2000).
 CC -!- FUNCTION: Oligomeric Apaf-1 mediates the cytochrome c-dependent
 auto-catalytic activation of pro-caspase 9 (Apaf-1), leading to the
 activation of caspase-3 and apoptosis. This activation requires
 Ap (By similarity).
 CC -!- SIMILARITY: Monomer. Oligomers upon binding of cytochrome c and
 caspase 9.
 CC -!- SIMILARITY: Cyttoplasmic (By similarity).
 CC -!- SIMILARITY: Contains 1 CARD domain.
 CC -!- SIMILARITY: Contains 1 NB-ARC domain.
 CC -!- SIMILARITY: Contains 13 WD repeats.

DR DR InterPro; IPR001315; CARD.
 DR DR InterPro; IPR002182; NB-ARC.
 DR DR InterPro; IPR001680; WD40.
 DR DR InterPro; IPR011046; WD40_like.
 DR DR Pfam; PF0619; CARD; 1.
 DR DR Pfam; PF00931; NB-ARC; 1.
 DR DR Prints; PR00400; WD40; 11.
 DR DR Prints; PR00320; GPROTEINBRAFT.
 DR DR ProDom; PD000018; WD40; 2.
 DR SMART; SM00114; CARD; 1.
 DR SMART; SM00320; WD40; 14.
 DR DR PROSITE; PS52209; CARD; 1.
 DR DR PROSITE; PS00678; WD_REPEATS; 1; 2.
 DR DR PROSITE; PS50082; WD_REPEATS; 2; 7.
 DR DR PROSITE; PS53294; WD_REPEATS; REGION; 1.
 DR DR PROSITE; PS53295; WD_REPEATS; REPEAT; WD repeat.
 DR DR PROSITE; ATP-binding; Repetit; WD repeat.
 DR DR CARD.
 DR DR ApoBiosis; ApT-Binding; Repetit; CARD.
 FT DOMAIN 106 417 NB-ARC.
 FT DOMAIN 106 417 NB-ARC.
 FT NP BIND 154 654 ATP (Potential).
 FT REPET 615 654 WD 1.
 FT REPET 657 656 WD 2.
 FT REPET 700 743 WD 3.
 FT REPET 746 785 WD 4.
 FT REPET 798 835 WD 5.
 FT REPET 840 879 WD 6.
 FT REPET 882 921 WD 7.
 FT REPET 964 1003 WD 8.
 FT REPET 1006 1045 WD 9.
 FT REPET 1047 1088 WD 10.
 FT REPET 1091 1130 WD 11.
 FT REPET 1133 1172 WD 12.
 FT REPET 1184 1223 WD 13.
 SQ SEQUENCE 1261 AA; 142933 MW; F80CC9CB41764F1C CRC64;

Query Match 55.7%; Score 3683.5; DB 1; Length 1261;
 Best Local Similarity 54.8%; Pred. No. 1.2e-05;
 Matches 691; Conservative 244; Mismatches 310; Indels 15; Gaps 7;

Qy 1 MDAKARNLLOREALEKDITKSYIMDMISGPLITSEKEVKNEPTQQRAMLIKMI 60
 Db 1 MEERARSRLRSKATKEQDIAKSYLMDDHMISGVLNDEAKVLSKATKEQAVALLETL 60
 Qy 61 LKCDNDSYVSFTNALHEGKDLAALHEGDPVYSSSGDSVSGITSVTVLCEGGVP 120
 Db 61 LRKDNRAYTVAJLIRESTGDLASLSDLSLSPGEKSFPADGVSPSVQALSVSGVP 120
 Qy 121 QRPVYFTRKLVNAIQOKLKSURGEPEPWHTHMGAGCGKSVLAAEVARDHSLECGFPG 180
 Db 121 LLDDWDSSWLKAFTSDQCLLTTROKSVTDVQDTPGWTYFGMAGSGSVMAEVWDRSLIKEFPD 180
 Qy 121 QRPVYFTRPILNIREMIXQDTPGWTYFGMAGSGSVMAEVWDRSLIKEFPD 180
 Db 121 YDYEALDEAMTSSEMLREIDKDYTDLSLUTRMLKRPFRS 238
 Qy 181 GHIVWVGDKQDSGLMQLNCLTRDODES-FSQRPLNTEAKDRIRLMLKRPFRS 238
 Db 181 GHIVWVGQCRADLVRQSLCPLRQCSQSDTSQRPPSTVEAKERIRLMLRPPR 240
 Qy 239 LL.LLDWDSSWLKAFTSDQCLLTTROKSVTDVQDTPGWTYFGMAGSGSVMAEVWDRSLIKEFPD 180
 Db 241 LL.LLDWDSSWLKAFTSDQCLLTTROKSVTDVQDTPGWTYFGMAGSGSVMAEVWDRSLIKEFPD 180
 Qy 241 YDYEALDEAMTSSEMLREIDKDYTDLSLUTRMLKRPFRS 238
 Db 361 YDYEALDAMASLQVLEAHQELYRDLSWMDQKDVTPARTVSYWGLELEBEVDLQEF 420
 Qy 419 VNKSLLPCDRGKSPRAYLHDLOQFUFTEBANSQDOLHKKITQFQYHOPHTLSPDQE 478
 Db 421 VNKSLLPCDRGKSPRAYLHDLOQFUFTEBANSQDOLHKKITQFQYHOPHTLSPDQE 478
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CC DR EMBL; AP251502; AA67189_1; -.
 CC HSSP; P16649; 1ERJ.
 CC ZDB-GENE-000616-4; apaf1.
 CC ZFIN; DSWWQFIPYHMAKGLSKLXYSLMFSLDWTEKARIMGSAAHLINDYVGBLTDKENS 540

QY	539 AVSENFOEFLSINGHILGRGPPNNIVOLGLCEPETSEVYQAKLQAKQEVDNGMLYLENI	RA Rahaa S.S., Louquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunnarane P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Ra Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahay J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Medan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeslee R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grubman J.W., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smalius D.E., Schnarch A., Schein J.E., Jones S.J., Marra M.A./
Db	541 EVRVOFELSLNGLHEQRPFDPDVQLLQDPRDEVRVQALMQRASRGQIYLNWV	RA
Qy	599 NKNNTNLRLYVPRPTDAVTHACRFEDQRIASCGADDTLQVPAETGKLLKEKAHD	RA
Db	601 NKNIEGLSLRYMPHQAVVYACTFKDGSKIASKGASKARLYFSTSGKELLELQABE	RA
Qy	659 EVLCCAFSTDRTFATCSVDRKVKLWNMTSBLVITYE-BHEEQNCCHPTNSHLLLA	RA
Db	661 DVLCCAFSPDDRHIACTSDRKVKLWNVERGYLIREFVEHQINHCQFTNGRVLIA	RA
Qy	718 TGSDDCP--LKLWDLNQKECRNTMFGHTNSYNTHCRSPDDKLASCSDA67KLWMDATAA	RA
Db	721 TCSNDPFTPLNPKTSNTMFHMEPMVNHCCEPNDLTLATSSDLSKLKEFVSSA	RA
Qy	776 NERKSANVNPQFLNLEDQPDQMEVYTKCWSMSADGARIWYAKNKFPLDIHTSFLGEGI	RA
Db	781 NEWKSDVYDSSPF--PESDEEIKAMYKCSWMSADQSQICARNTVVFDEVTSUILLKL	RA
Qy	836 HTGHHRHTIYQCDESPONHALVAVSCLWVYDTRGHLSTWGMWSPDSG	RA
Db	838 KTSRLSTIQFCHACPNSSLALAVASHYTTELWNPESSKKCAECSSHLSWTHCQFSPDSG	RA
Qy	896 SFLTSSDDOTIRLWETKVKCCKNSAVALMKOEVYDYYPOENETMVLAVDHIRRQLQINGRTGQ	RA
Db	898 DLLSSDDOTIRLWETDRAVTPSSAVALKRDTDVLSHSATIADDSSNRLQVLGSGTA	RA
Qy	956 IDYLTE--AQVSQCCCLSPHLOQIAYFGDENGAIETLEVNRRIFOSRFQHKKTWHIQFT	RA
Db	958 VVLESELSSRRCSCTRNAFAVLAGSEDTQVIBEVPSKSKASVYKLSGTITVHCOFT	RA
Qy	1013 ADERTLISSSDAEIQNWNLWDKTFDRFLJKNS--RLLJSWSFGTVKV 1069	RA
Db	1018 DDCELIITSSSDSTRWKWRTGECHVQLGIMEPYRKFHILLSSSSPHFLWSFGTVKV	RA
Qy	1070 WNIITGNKEKDFVCHQGTVLSCDISDATKPSSTSADAKTAKWSPDLLPLHRLRGHNAC	RA
Db	1078 WDLTRQMLQDPLVCHGAVLSCDVSSDGRIFATTSAANRATKWMWSASWKNLFLIGHKDC	RA
Qy	1130 VRCSAFAVSDTLLATEDDNGBIRIWNNGELHICAPLSEGA-ATHGWWTDLCFSPD	RA
Db	1138 VRSCRFSDWNKRLLATDDNGEIRLWSMGLALLKICPRDKDSMNSYHAGWWTDLHFSPD	RA
Qy	1189 GRKMLSAGGYIKWWVNVVTGEESQSFYFTNGTMKIKHVSPEDEKTYTVDNGILYLTQLE	RA
Db	1198 NRVLNSTAGIJKWWVSEGEALQFTYMGGNLKKIHVSPDDESTFTVDSIGILYLRLE	RA
Q80VRS	PRELIMINARY;	RESULT 7
ID	Q80VRS	Q80VRS
AC	Q80VRS;	SEQUENCE FROM N.A.
DT	01-JUN-2003 (TREMBLrel. 24, Created)	RC TISSUE=Olfactory epithelium;
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)	RX MEDLINE=2238257; PubMed=12477932;
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)	RA Strasbourg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D., Altschul S.F., Zeeberg B., Bustow K.H., Scheffer C.F., Bhat N.K., Hopkins R.F., Jordau H., Moore T., Max S.I., Wang J., Heish F., Diatchenko L., Marusina K., Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Muridae; Murinae; Mus. NCBI_TaxID=10090; [1]
RN	RP SEQUENCE FROM N.A.	OC TISSUE=Olfactory epithelium;
		RX MEDLINE=2238257; PubMed=12477932;
		RA Strasbourg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D., Altschul S.F., Zeeberg B., Bustow K.H., Scheffer C.F., Bhat N.K., Hopkins R.F., Jordau H., Moore T., Max S.I., Wang J., Heish F., Diatchenko L., Marusina K., Iriuchi M., Nakamura Y., Kuritz T., Watabane A., Kohara M., Ishikawa A., Kawashima K., Kimura T., Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
		OC TISSUE=Olfactory epithelium; Nostocaceae; Nostocales; Nostoc; NCBI_TaxID=10690; [1]
		RP SEQUENCE FROM N.A.
		RX MEDLINE=2159585; PubMed=11759840;
		RA Kaneko T., Nakamura Y., Wolk T., Kuritz T., Sasamoto S., Watabane A., Iriuchi M., Nakamura Y., Kuritz T., Watabane A., Kohara M., Matsunoto M., Muraki A., Kishida Y., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
		RA

Yasuda M., Tabata S.; "Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120."; DNA Res. 8: 205-213 (2001).
 -1-
 EMBL: AP003581; AE18103;
 DR: PIR: AE1810.
 HSPB: P16649; IERU.
 GO: GO:0005622; C: intracellular; IEA.
 GO: GO:0005524; F: protein binding; IEA.
 GO: GO:0032700; F: transcription factor activity; IEA.
 GO: GO:0008915; P: apoptosis; IEA.
 GO: GO:0012829; P: defense response to pathogen; IEA.
 GO: GO:0006355; P: regulation of transcription, DNA-dependent; IEA.
 InterPro: IPR009505; bi resp regltr C.
 InterPro: IPR011048; CyF_cdl_hemC.
 InterPro: IPR007677; Disease_resist.
 InterPro: IPR002196; HTH_Fis.
 InterPro: IPR000793; HTH_LuxR.
 InterPro: IPR002182; NB-ARC.
 InterPro: IPR001680; WD40.
 Pfam: PF00931; NB-ARC; 1.
 Pfam: PF00401; WD-40; 14.
 PRINTS: PRO0364; DISEASERS1ST.
 PRINTS: PRO0320; GPROTEINBP7.
 PRODOM: PD000018; WD40; 13.
 SMART: SM00320; WD40; 14.
 TIGRFAMs: TIGB01199; HTH_Fis; 1.
 PROSITE: PS00678; WD_REPEATS_1; 12.
 PROSITE: PS00822; WD_REPEATS_2; 14.
 PROSITE: PS00594; WD_REPEATS_REGION; 1.
 Complete proteome; Repeat; WD repeat.
 SEQUENCE: 137235 AA; 137235 MW; 466P26939ED4FBP CRC64;

 Query Match Score 732; DB 2; Length 1227;
 Best Local Similarity 22.2%; Preq. No. 1e-33; 384
 Matches 295; Conservative 29; Mismatches 438; Indels 384

 Qy 77 HEGYKDAAHLHIGIPVYVSSSSGKDSVSGITSYRTVTCGGVPQRPVVVFVTT
 SO 45 HSG-REIAKRLDTSQPAVRKGEE-----SI-RKLGIEG-----KCI
 DR 137 QQLSK-----LKGEPW-----
 DR 86 RQKLYEQYQLSYQHPVSSEDGAEAVDAGFRGRKEPILEQWIEGNGNSNR
 DR 155 MAGCKSKVLAEARV-----DHSLLEGCPGGVHWVSGKDKDGS-LIMKLK
 DR 146 MGGKCTVLAAMAKVQKEPDYL-----WESLRVNPAPSGLDITIOLII
 DR 208 QDEPSFSQLRPLNIEEAKDRFLRMLRKPHRSLLJDDYW-----DSW
 DR 196 END-----LTDNNKKIVRLIDVLKRKCLLIDNNEVSIRSGEKNOQEWAA
 DR 250 -----VLFKAFCQGCFDQKTSVDSWGPCKVYVPESSIGKEKGK
 DR 249 ENYGYLFKVAELASHESC-LILTSREK-----PREVALE--GKNLPV
 DR 300 NMKCAD-----LPEQHSAIIKECKGSPLVSLGALLRD-FPNWVEYY
 DR 297 NLAEREIILDKGAFYCDEQDDELTVRYGKQNLALKVATVTFNSNNE
 DR 345 -----LQNQKOPKR---TRKSSSDYEALEDAAMSISVEMLREDIKOYTT
 DR 357 SAVXGDIRTLKQFQRLUSELKKYMSLGANREYVS-----FRELKDOWLT
 DR 393 VKVPTPKVCLIWDMETREVIDLQEFV-----NKSLLFCURNGKSFR
 DR 407 -----BALESILRSLLIEKAASFTLIEKAASSTGKEAASSSK
 DR 443 DFLTERNSSQLDQHKKITQRVHQPHLSPQEDMWNYNFL-AYMAMSA
 DR 456 EYIT-----KTESENLESESQTCKL
 DR 457 DFLNTYPLMKZ

RESULT 9					
		YSPO ANASP	STANDARD:	PRT:	1258 AA.
Qy		Y8YTC2;			
Db		AC	(Rel. 41, Created)		
Qy		Y8YTC2;	28-FEB-2003 (Rel. 1, Last sequence update)		
Db		AC	05-JUL-2004 (Rel. 44, Last annotation update)		
Qy		Y8YTC2;	Hypothetical protein air2800.		
Db		AC	Order:redLocusName=air2800;		
Qy		Y8YTC2;	Anabena sp. (strain FCC 7120).		
Db		AC	Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.		
			SEQUENCEID=21592285; PubMedId=11759840;		
			LINEID=103690;		
			LINEID=111;		

RA	Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Watanabe A., Iriuchi M., Ishikawa A., Kawashima K., Kimura T., Kohara M., Matsunoto M., Matsuno A., Muraki A., Nakazawa N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S.	386 SQQPIFDDIDRLDQQFQLTLEIREINWLA-NREPUYLAELQADFVANIPPRELLE 445
RA	"Complete Genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PC-7120."	414 ILQEFNKSILFCDCNGKSPRYLLDQVDFLTENCSQLD---LHKKIIITQYHQ 469
RT	DNA Res. 8:205-213(2001).	446 SLSSLORRSLEKSGCGFTIOPPVMEYVSNHLIBOVCBEEREWGLYRSRGAEBQSRSGEK 505
RT	-! SIMILARITY: Contains 1 NB-ARC domain.	470 PHTLSPDQEDCMYWNFLATHMASAKOMKHKECLCALMFSLD-WIKATELYVPAHLTHEFVE 528
CC	CC -! SIMILARITY: Contains 15 WD repeats.	506 INT-----QYKLNALPLTLASTPFTTHALKAKRK-----DVYR 541
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	529 YRHILDEKDCAVSENQEQFISLNQ-----HILGQPPPNIVQLGICPEPETSEVYVQAKL 582
CC	CC	542 ESQISLILQPHINOLJTEPESLLENNSNCLVHLSLRGSPQETSYAGGNVNLHHAQV 601
CC	CC	583 QAKQEVNDNGM---LYLEWINKNQ---TNLSLRLVPRPTDAYHACFSDFGORIASCG 634
CC	CC	602 DLSGVDTSGLTVWQAYLGQVNLDYDFAINSDLSCCVFTETLGNIISAAFSPEGQLIATCD 661
CC	CC	635 ADKTLQVPKAETGEKULLEKAHDENVLCACAFSTDDRFIATCSVDPDKVKWLNWSMTGELVHT 694
CC	CC	662 TDCHYRWEYRSKLLICRGHSNMNVRFFVSPDDEBILASGADDNVLKMSVDRDVCIKT 721
CC	CC	695 YDEHSEQVNCCFHFTSHILLATCSDCEFLKWLMLNQRECRNTMFGHTNSVNHCFSPD 754
CC	CC	722 LTGHHEBEVFSVAFHEDGE--TLASASGDKTIKLWNIODGTCLQTLTGTDWVRCYAFSPD 779
CC	CC	755 DKLJASCSADGTLKWLDSANERSINVKOFFNILEDPODMEYVTKCCSWASADGARIM 814
CC	CC	780 GNTLASSAADHTIKWDVSOKCLTSLKSHTGW-----VRSVAFSAQGOTLA 826
CC	CC	815 VAAKNIK-IEFLDIHPSGLGEIHTGHSHSTIQCQCDSPONHLLAVVVAISLQCYCVELANTDSRS 873
CC	CC	827 SGSGRTIKIWNHYHTGECL-KTYIGHNTNTSYSIASPSDKSILVSSGSDRITKLWICQTHI 885
CC	CC	874 KVADERGHISWVHGGMFSPDGSSFLITSDDQTIRMETKVKCNSAVMLKOEVDVVFQEN 933
CC	CC	886 CIKTLHGHNTNBVCSTAFSPDQTLACVSLDQSVRWN----CRTG----- 926
CC	CC	934 EVMVIAVDHTIRRLQIINGRTQIDLTAEQVSCCLCSPHIIQYTAGDENGAIIEIILVNN 993
CC	CC	927 -----QCLKAWTGYNTDIALPV-----AFSPDRIQLAGSNDKTVKLWDWTQG 968
CC	CC	994 RIFQSRFOHKTKVWHIQFTADEKTUJISSDDAEIQTYWNWQLDKC1-FLRQHQTVDFRL 1052
CC	CC	969 KYISSELEGHTDFIYGLAFSPDSQTLASASTDSSVYLWNISTGQCQILLDHTDWYAVFV 1028
CC	CC	927 -----QCLKAWTGYNTDIALPV-----AFSPDRIQLAGSNDKTVKLWDWTQG 968
CC	CC	994 RIFQSRFOHKTKVWHIQFTADEKTUJISSDDAEIQTYWNWQLDKC1-FLRQHQTVDFRL 1052
CC	CC	969 KYISSELEGHTDFIYGLAFSPDSQTLASASTDSSVYLWNISTGQCQILLDHTDWYAVFV 1028
CC	CC	1053 LKNSSL-SWSFDPGTVKWNITIGNEKEKDPVCHQGTVLSDISHATKFSSTSADKTAI 1111
CC	CC	1029 HPOGRKIAITGSSADCTVKLNNISTGCQLKTLSEHSDKILGMAWSPPGQLLASASADQSVRL 1088
CC	CC	1112 WSFDLILPHBLSTULGTDNGEIRIWNNGELLHLCPALSER 1171
CC	CC	1089 WDCCTGRCVGULGRGSNRVYAFSPNGEIAITCTDTQTKWIDVQGKCI-----K 1140
CC	CC	1172 GAATGGWWTDLCFSPDGKMLISAG-GYKWWNNVVTGESSQTFYTNGTNLUKKTHVSPD 1228
CC	CC	1141 TLTRGHTNWVFDIAFPDGKILASASHDQTRWIDNTGKCHHICGHTHLVSSVAFSPD 1199
CC	CC	RESULT 10
CC	CC	Q7ND85 ID Q7ND85 PRELIMINARY; PRT; 1184 AA.
CC	CC	DB
CC	CC	224 LIQFELSGQETNLS-NHLQRISLILKLNRSRCLLIDNA-BSLQAGDNRGYRAGC 280
CC	CC	256 -----SQCQILITTRDKSVTDSVMG-PKY--WVYES----SLGKEKGLE 293
CC	CC	281 EGYGFQFLQCIATSHQSCLITTSREXP----QHAKYEGDSLPRSLPLTGQEOQEGR 335
CC	CC	294 ILSLFVNMMKADLPBEAHASLIKCKGSPLVYSLIGALLRDPNREYKYLQLQNQFKRI 353
CC	CC	336 LFN--VKGKPAASCDCOWQVLISRGGNPALKIVASSIRDEFDG-----DVSQFLEY 385
CC	CC	354 RKSSSYDYEALDEAMSISVEMLREDIKYDYYTDLSTLQKDVKVPTXVLCILWDMETEEVED 413

SEQUENCE FROM N.A.	
STRAN-PCC 7422;	RP
MEDLINE=P-22377005; PubMed=14621292;	RC
Nakamura Y., Kaneko T., Sato S., Miyashita H., Tsuchiya T.,	RX
Kohama S., Watanabe A., Kawasaki K., Kishida Y., Kiyokawa C.,	RX
Kohama M., Matsumoto M., Matsuno A., Nakazaki N., Shimono S.,	RX
Takeuchi C., Yamada M., Tabata S.;	RX
"Complete genome structure of Gloeobacter violaceus PCC 7421, a cyanobacterium that lacks thylakoids.";	RX
DNA Res. 10:137-145 (2003).	RX
[+ SIMILARITY: Contains 14 WD repeats.	RX
EMBL: AP00583; BAC9292.1; -.	RX
GO: GO:0005524; F:ATP binding; IEA.	DR
GO: GO:0005915; P:apoptosis; IEA.	DR
GO: GO:0043829; P:Defense response to pathogen; IEA.	DR
Int-Pro: IPR000767; Disease_resist.	DR
InterPro: IPR002182; NB_ARC.	DR
InterPro: IPR001680; WD_ARC.	DR
Pfam: PF000431; NB_ARC; 1.	DR
Pfam: PF000430; WD40; 14.	DR
PRINTS: PRO036; DISEASEB1ST.	DR
PRINTS: PRO3220; GRINTEINBPT.	DR
Prodrom: PD000018; WD40; 13.	DR
PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_7.	DR
PROSITE: PS50082; WD_REPEATS_2; WD_REPEATS_1.	DR
PROSITE: PS50294; WD_REPEATS_2; 14.	DR
PROSITE: PS50294; WD_REPEATS_2; WD_REPEATS_1.	DR
Complete protein; Repetition; WD repeat.	DR
SEQUENCE 1184 AA; 128483 MW;	DR
Score 693; DB 2; Length 1184;	Qy
Best Local Similarity 23.8%; Pred. No. 1.8e-31;	Qy
Matches 275; Conservative 172; Mismatches 469; Indels 238; Gaps 36;	Qy
150 VTIHAGGCKSVTAEEAVRDISSLSCPGVHIVSVKGKQDSGLIMKLNQNCVRLLDD 209	Qy
138 VAVLNGGCKTAAVKLAROS--DAHFERLIIWRSL--RNAPPLADLAEELITVAGD 191	Qy
210 EFSQRQLNIEAKDRRLMLRKHPRSLIILDDWDWSWIK-----AFDSQQ----- 259	Qy
192 Q--APALPTGIE--IIRLCLQRNRCVLLDRA--ESLRLGGBAGTYREGEGYGR 245	Ddb
260 -----ILLTRDRKSVDTSVMGPXVYVPESSLGKEKGLEIISLFWNMNKKADL 306	Qy
246 LIRRGEVPHASCLVLSREK-----PAEVAALEGSSLPVSRRLGGI---QESEGV 295	Ddb
307 PEQANSI-----IKEC-KSPLYVLSSLLGALLR--FPNMEYLQ-----L 345	Qy
296 IIAQKLGKGADEERKLVBCYRGNPALMISTIESTFDFGQIREFLAQDTAVFGIANI 355	Ddb
346 QNKOKRIRKS-SSYDFALDBAMSISVEMREDIKDYTDLSILQDKVYPTKUCLCW 404	Qy
356 LQQQDPDLTEAKOLMYWLAHREPVTAVQREN-----VPA----- 393	Ddb
405 DMETFEVDLTLQF3VNSKLLFCDRNGKSFRYQHLQDLOVDELTENCSQSOLODLHKCITOF 464	Qy
394 -VSAPKILEASLRLSLIERGTTGYSQQPVNEYTEHFYIC--DEVHKTGIF 449	Ddb
465 QRYHQHPLSPDQEDCMWNFLAYMAMHHMKBLCALMFSLWIKAKTELGVPHLH 524	Qy
: RSH-----ALLAQK-----DYLRAAQSRLTIKPVID 477	Ddb
525 EFP---EVHILDEKCAVSENQFQLSLNHGLROPPNIVQGLCEPETSEVYQA 580	Qy
478 BLVRLIGSQAH----EQRLLAVALQDOPQTVGGNTL--NMNLATLQTELRHWFSLHA 535	Ddb
581 KIAQAKEVQDNGMYLEWINKNI---TINSLRVLVRPHTDAYHACFSESDQORTASCGAD 636	Qy
536 WQA-----YLOENLQKVNFWFHDLARCIAFNQEGGVFSVAFSPDQIAVGDN 586	Ddb
637 KTLQVEKAETGEKULEKIAHEDBVLCACFSTDDFLAICSDVKKVIWNSMTGELVHTYD 696	Qy
587 SEIRUWRAADQOQLSCQGHTDWCAVAPAFNGCTEASASQGTWLWDRIGOCCLTLR 646	Ddb
697 EHEQVNRCHEFTNSHLLATATGESSCDFLKWDLNQECRTNFMGHTSVNHCRCSPDK 756	Qy
647 GHIGWRSAAFPDGs--LIA\$AGQDSTVKLMDAATGRCLATLQGHTGVHSVAFADGS 704	Db
757 LIASCSADGTLKLWATSAERKSINVQFFNLNEDQEMEVTKVCCNSAWGDARIMVA 816	Qy
705 LIASAGQDSTVKLWDATG-----RCIA----- 727	Db
817 ARKNIKLFIDIHTSGLGEIHTGHSHIOYCDPSPNLHAVALSOYCVELWNTDSRSKVA 976	Qy
728 -----TLOQHEBPIRSVVSPOGHRSLASAHSRTRYLWNPATGRCLC 769	Db
877 DCRGHLSWVHGVMSPDGSSPLTSIDOTIRMETKVCNSAIVMLOKEDVUVFO----- 931	Qy
770 TLZLGHGDWVSAVAPPDGRSLANGSLDRTVLINE--ITSGQCLKLQEHTDQVSIAFPHP 827	Db
932 -----BNEYNVLAVIDHIRRLQJLNGTQDYLTEAQVSCCILSPHOIYARGDE 981	Qy
828 QCHTLAGSASGSPQTQVTLWDMTESGQCLRLTQGKD-----VTVLAVAFSPHGTGTLVGSGD 879	Db
982 NGIEELLEVNRLRIFOSRFOHKKTTWHIQFADETLISSSDABEIQWNNQLDKC1--FL 1040	Qy
880 DRIVRVLWDVTCGECTRVLRGLGTVTAVAPDGTRLASAGDLISKV1WDLSQGCLRTL 939	Db
1041 RGHQETVKDFDALLKNSRLI-SWSFGTVKVNNLITCNKEDFVQHGTVLSCLSDHDATAK 1099	Qy
940 RETGCSRSDVAFDORLIAASQDGTAKLNDPGRCTVATLQHSPKTSIAFADGGL 999	Db
1100 FSTSADKTAIWSPDILIPHLIRGNGCVRSACFSVDTLIAITGDNDETRWVNSG 1159	Qy
1000 LASGSQDGTATARIWDTGRCLQLAGTYLICSVASFLSDQLLASGSDQDTIRLWVQGT 1059	Db
1160 EHHLCAPISLSEGAAATHGGWYDLCFPPDGKMLISAGG--YIKWNVTVTGESSQTFYTNG 1217	Qy
1060 ACIR--TLETKI--TSMVFSLAFSPDGQILASGSNDMTVTLWQVTGRCVKTIGPHT 1111	Db
1218 TNLKKTHVSPDPEKT 1231	Qy
1112 SLVSVIAYAPGST 1125	Db
RESULT 11	
YY46 ANASP STANDARD PRT; 1526 AA.	
ID YY46 ANASP	
AC QBTRII;	
DT 05-JUL-2004 (Rel. 41, Last sequence update)	
DT 28-FEB-2003 (Rel. 41, Last annotation update)	
DE Hypothetical WD-repeat protein alr3466.	
GN OrderOfCdsName=alr3466.	
OS Anaebna sp. (strain PCC 7120).	
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.	
RN NCBI_Taxid=103690;	
RP SEQUENCE FROM N.A.	
RX MEDLINE=2115255; PubMed=11759840;	
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,	
RA Watanabe A., Iriuguchi M., Ishihara K., Kawahima K., Kimura T.,	
RA Kohida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,	
RA Nakazaki N., Shimpou S., Sugimoto M., Takazawa M., Yamada M.,	
RA Yasuda M., Tabata S.,	
RT "Complete genomic sequence of the filamentous nitrogen-fixing	
cyanobacterium Anabaena sp. strain PCC 7120";	
RL DNA Res. 8:205-213(2001).	
CC -! SIMILARITY: Contains 1 pentapeptide repeat domain.	
CC -! SIMILARITY: Contains 16 WD repeats.	
CC This SWISS-PROT entry is copyright. It is produced through a collaboration	
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -	
CC the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way	
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EMBL; P003593; BAB75165_1; -	NEPLIKKIE 796
PIR; AC2239; AC2239.	SEFLDKLRETRCKAKLTKAVIDLPLLPMDD;
HSSP; P16649; 1ERJ.	556 L--GLCPETSEVYQQAK-----NIT--NLS 607
InterPro; IPR007111; NACHT_NTPase.	797 ATRGRTEDEVNYGGNRAATLVLVKLNKMLVGRDLSSHTVIAGDFTTNLSRCVNFTANLA 856
InterPro; IPR0011047; Quin_acic_DH_like.	608 RLYVRPHFTDAYHACFSEDGORIASCGADKTQLQVFAETGELLETAHEDEAFLCAFST 667
InterPro; IPR001680; WD40.	857 YSVPTKILGSVLTVAFSPDGKLFASTDGG1VRFWEATGKLLTKGHNSWNSVGSFSQ 916
PRINTS; PRO0320; GPROTEINBRPT.	668 DDERFLATCSDVKKVWKIWNMSMTGELYWHTYDSEHSEOVNCCHFTNSHHILLATGSSCDFLKL 727
Prodom; PD000018; WD40; 8.	917 DGKMLASGSDQTVRLWDISSGQCLXFKGHTSRVSVFPNS - LMLASGSDDQTVRL 974
SMART; SM00320; WD40; 15.	608 RLYVRPHFTDAYHACFSEDGORIASCGADKTQLQVFAETGELLETAHEDEAFLCAFST 667
PROSITE; PS50837; NACHT; UNKNOWN 1.	857 YSVPTKILGSVLTVAFSPDGKLFASTDGG1VRFWEATGKLLTKGHNSWNSVGSFSQ 916
PROSITE; PS00678; WD_REPEATS_1; 11.	668 DDERFLATCSDVKKVWKIWNMSMTGELYWHTYDSEHSEOVNCCHFTNSHHILLATGSSCDFLKL 727
PROSITE; PS502984; WD_REPEATS_2; 15.	917 DGKMLASGSDQTVRLWDISSGQCLXFKGHTSRVSVFPNS - LMLASGSDDQTVRL 974
Complete proteome; Hypothetical protein; Repeat; WD repeat.	728 WDLNQKECRNTMFGHTNSVNHCRSPDDKILASCADGTKLWMDATSA-----NE 777
REPEAT 334	928 WDLNQKECRNTMFGHTNSVNHCRSPDDKILASCADGTKLWMDATSA-----NE 777
DOMAIN 823	928 WDLNQKECRNTMFGHTNSVNHCRSPDDKILASCADGTKLWMDATSA-----NE 777
REPEAT 862	928 WDLNQKECRNTMFGHTNSVNHCRSPDDKILASCADGTKLWMDATSA-----NE 777
REPEAT 862	928 WDLNQKECRNTMFGHTNSVNHCRSPDDKILASCADGTKLWMDATSA-----NE 777
REPEAT 904	928 WDLNQKECRNTMFGHTNSVNHCRSPDDKILASCADGTKLWMDATSA-----NE 777
REPEAT 946	928 WDLNQKECRNTMFGHTNSVNHCRSPDDKILASCADGTKLWMDATSA-----NE 777
REPEAT 985	928 WDLNQKECRNTMFGHTNSVNHCRSPDDKILASCADGTKLWMDATSA-----NE 777
REPEAT 988	928 WDLNQKECRNTMFGHTNSVNHCRSPDDKILASCADGTKLWMDATSA-----NE 777
REPEAT 1027	928 WDLNQKECRNTMFGHTNSVNHCRSPDDKILASCADGTKLWMDATSA-----NE 777
REPEAT 1030	928 WDLNQKECRNTMFGHTNSVNHCRSPDDKILASCADGTKLWMDATSA-----NE 777
REPEAT 1069	928 WDLNQKECRNTMFGHTNSVNHCRSPDDKILASCADGTKLWMDATSA-----NE 777
REPEAT 1072	928 WDLNQKECRNTMFGHTNSVNHCRSPDDKILASCADGTKLWMDATSA-----NE 777
REPEAT 1111	928 WDLNQKECRNTMFGHTNSVNHCRSPDDKILASCADGTKLWMDATSA-----NE 777
REPEAT 1114	928 WDLNQKECRNTMFGHTNSVNHCRSPDDKILASCADGTKLWMDATSA-----NE 777
REPEAT 1153	928 WDLNQKECRNTMFGHTNSVNHCRSPDDKILASCADGTKLWMDATSA-----NE 777
REPEAT 1156	928 WDLNQKECRNTMFGHTNSVNHCRSPDDKILASCADGTKLWMDATSA-----NE 777
REPEAT 1195	928 WDLNQKECRNTMFGHTNSVNHCRSPDDKILASCADGTKLWMDATSA-----NE 777
REPEAT 1198	928 WDLNQKECRNTMFGHTNSVNHCRSPDDKILASCADGTKLWMDATSA-----NE 777
REPEAT 1237	928 WDLNQKECRNTMFGHTNSVNHCRSPDDKILASCADGTKLWMDATSA-----NE 777
REPEAT 1240	928 WDLNQKECRNTMFGHTNSVNHCRSPDDKILASCADGTKLWMDATSA-----NE 777
REPEAT 1279	928 WDLNQKECRNTMFGHTNSVNHCRSPDDKILASCADGTKLWMDATSA-----NE 777
REPEAT 1282	928 WDLNQKECRNTMFGHTNSVNHCRSPDDKILASCADGTKLWMDATSA-----NE 777
REPEAT 1282	928 WDLNQKECRNTMFGHTNSVNHCRSPDDKILASCADGTKLWMDATSA-----NE 777
REPEAT 1321	928 WDLNQKECRNTMFGHTNSVNHCRSPDDKILASCADGTKLWMDATSA-----NE 777
REPEAT 1324	928 WDLNQKECRNTMFGHTNSVNHCRSPDDKILASCADGTKLWMDATSA-----NE 777
REPEAT 1363	928 WDLNQKECRNTMFGHTNSVNHCRSPDDKILASCADGTKLWMDATSA-----NE 777
REPEAT 1366	928 WDLNQKECRNTMFGHTNSVNHCRSPDDKILASCADGTKLWMDATSA-----NE 777
REPEAT 1405	928 WDLNQKECRNTMFGHTNSVNHCRSPDDKILASCADGTKLWMDATSA-----NE 777
REPEAT 1408	928 WDLNQKECRNTMFGHTNSVNHCRSPDDKILASCADGTKLWMDATSA-----NE 777
REPEAT 1447	928 WDLNQKECRNTMFGHTNSVNHCRSPDDKILASCADGTKLWMDATSA-----NE 777
REPEAT 1450	928 WDLNQKECRNTMFGHTNSVNHCRSPDDKILASCADGTKLWMDATSA-----NE 777
SEQUENCE 1526 AA; 170376 MW; DSDP272509BA738 CRC64;	928 WDLNQKECRNTMFGHTNSVNHCRSPDDKILASCADGTKLWMDATSA-----NE 777
Query Match 10-4*	Score 691; DB 1; Length 1526;
Best Local Similarity 22.1%; Pred. No. 3.5e-31;	Db 1260 GSSDKTVRLWDISSSKCLHTFQGHITWVNSYAFNPDDGSMLASGSDQTIVRIWEISSSKCL 131
Matches 286; Conservative 238; Mismatches 530; Indels 240; Gaps 44;	Qy 1039 F-LRGHOETVYDFRLLKNSRLL-SNSFDGTVKWMNLITGNKEKDVFYCHGOTVLSCIDISHD 109
104 SGITSYTVLCEGGVQRPVVFVTRKLVNAIQOKK--LSKLKGEPGVTHGMAGCGK 160	Db 1320 HTFQGHITWVNSYAFNPDDGSMLASGSDQTIVRLWISSGECLYTFLIGHTNNGVSIFPSD 1377
310 SCYDWWBAAETKRKRKDQKXPLACTKEIDPVTRKRIGSRYEADGWGDGY-----I 363	Qy 1097 ATKFSTSDAKTAKWSFDLPLIHLRGANGCVRSASFUDSTILATGDDNGEITIWN 115
161 SVLAAEVARDHALLGECPGGVHWVSVG-----KQDKSSLLMKLQLNC 203	Db 1380 GAILASGSDDQTVRLWISSSKCLHTFQGHITWVNSYAFNPDDGSMLASGSDQTIVRLWNI 143
364 DLWLDDPAKEHISTLGFBGTGKTFWVHYAWTAQLORYKDAQRQGVVERPLPVLTIRFDA 423	Qy 1157 SNGELLHLCAPLSEGAAATHS--GWTDLCSPDGGKLISAGG--YIKWWANVVTGESSQT 121
204 TRLDDE-----SFSQ--RLPLNTEAKDRILML-----RKPRSLLTDVW 246	Db 1440 SSGECLY-----TGHINHSURSVAFSSDGLILASGSDDDETIKLWDVKTGEICKT 148
424 KALNVENVLAGFFTORINRINSEVDFQLNRNGKLLIFDGFDEMAKVDQOMT -NNFW 482	Qy 1213 FYT----NGTNLKKIH-----VSPDFKTYTVDN 1237
247 DSWLKLAFDSQCQILITTRDKSVTDSUMGPKVY-VPVESSLGKEKG---LEILSL--- 297	Db 1490 LKSEK1YEGMNITSVRLTEVEATLKLTLGAVEN 1523
483 E--LAKVYVGPSKVLITWDMDEEEVDTQPEAKRGRNAAELQASTNKLTQETPOPEVLELEKFN 540	RESULT 12
298 FVNMKKADLPQAHSLIKKEKGS-----PLVVSIGALLRDP-----NRMEYKL 343	Q7NJ67 PRELIMINARY; PRT; 1197 AA.
541 DEQIROVLYQAEATEVQINGNSQQLDARRPMTDLEALPDTEAGKPIDMSRVLY 600	ID Q7NJ67 ID Q7NJ67; AC Q7NJ67;
344 QLQNQKPFKIRKSSSYD-----YEALD-EAMSISVEMLRDIDKYYTDSL 389	DT 01-MAR-2004 (TREMBLrel. 26, Created)
601 AVRKHMERDIKAERTFNSLADKLYPLCLESWMLSTDQMSLNRYLPERFLRLFG--SVV 658	DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
390 QKDVKVPTKVLCILWDMDEEEVDTQPEAKRGRNAAELQASTNKLTQETPOPEVLELEKFN 549	DE WD-repeat protein.
659 Q-----BEKOLDHWWYDMAQTMLYRNADG-DYTPAHRSSLEFFVAYKF 701	GN OrderedLocusNames=g1r1965;
OC Bacterium cyanobacteria; Cyanobacteria; Chroococcales; Gloeobacter.	OS NCBI_TaxID=33072;
RN [1]	RP SEQUENCE FROM N.A.
RC STRAIN=PCC 7421;	RA PMID=14621292;
RA Nakamura Y.; Kaneko T.; Sato S.; Miyamoto M.; Miyashita H.; Teuchiya T..	RA
450 CSQOLDIHKKI--ITOPQRYHOPHTLSPQEDCMYWNFLAYHMASAKMKELCAL-MFS 506	
702 AAEGLALARDFEVGQAQSGLDSSTSADYT---WGGYFSRQLDSTGGCREVIAPIRQFK 757	
507 LDWIKRATKTELGVPAH1IHEFV-YRHLDEDKCAVSENFOEFLSLNGHLLGROPPENIVQ 565	

Query Match	10.2%	Score 677.5; DB 2;	Length 1711;	Qy	825 DIHTSGLGLAEIHTGHHTIQCDSPTQHNLKAVVLSQCYCVELWNTDRSRSKVADCGHLSW 884
Best Local Similarity	22.8%	Pred. No. 2.5e-30;		Db	1298 S--RNGTLLTLEGENEATWQVISPDGRLIATASADKTITLWSRDG-NILGTAGHNHE 1354
Matches 322;	Conservative 248;	Mismatches 52;	Indels 315;	Gap 64;	
7 NC1QHREALKEIDIKTSYIMDHMISDGTLTSEEKYVNEPT-----QQ 51				Qy	885 VHGVMFSPDGSFLSTSDDOTIRLWETKEVKNSAVMLKQEVDFVYFQENR---VNVLAVD 941
359 NC-LOSERE-LETENQNQLATTIL--YLRGKLAESPTGEPLVGENITQLNRSWLRQL 413				Db	1355 VNSLJSFDNIALGSDDNTRVLTWQVISPDGRLIATASADKTITLWSRDG-NILGTAGHNHE 1354
52 RAAMLIMIL---KCONDSYSFYNALLHEGYKDANLHDGIPVSSSGKDSVSGIT 107				Qy	885 VHGVMFSPDGSFLSTSDDOTIRLWETKEVKNSAVMLKQEVDFVYFQENR---VNVLAVD 941
414 RESLYSKQIIFPDCPKJHSYS---LQDWYEDLQIGEFOQCITIAASSPENPQQL 468				Db	1355 VNSLJSFDNIALGSDDNTRVLTWQVISPDGRLIATASADKTITLWSRDG-NILGTAGHNHE 1354
108 SYVRTVL-----CEGVVPORVVFTTRKLVNA 135				Qy	942 HIRHLQLINGRTGQIDYLTEAQVSCLSPHLOYTAFGDENGATILEVNNR---IQFS 998
469 QTHLSTLQAHQEQOPNLSAAWINQLOQSSPLPHIWLSSGAKVIEITIPASTDAKGKRPNA 528				Db	1415 STMKTMWSLDCKLGLTSSPLPDVTSISFTPDNKLVALASPDHTHLY---NRQGCLLRS 1470
136 I-----QKQSLSKLKGEGPKGVNTVINGMAGCKSV---162				Qy	999 RFOHKKTVWHIQFTADEKTLISSDDAEIQW---NWQLDKCIFLRGHQETVQDFRLLKNS 1056
529 IVDLGICPYRGQIAQFQEDVOYFYGRETLTQOLIADLANK-SEMAVYGAASSGCKSSVYQA 587				Db	1471 LPGHINHWITSLSFSPNKQIASSADKTITLWSRDG-NILGTAGHNHE 1528
163 -LAEEAARDHDSLLEGCFFPGGGHVVSVGKQDKSSELMQLN-LCTRLDODESPSQRPLIN- 219				Qy	1057 R-LIISWFSDGTWVKNLITGKNEKDFVCHGTVLSCDISHDATEFSSTSADKTAKWSD 1115
588 GLIAQLRQQL---PGSQETWMKSPRPGPEPVLSHSKCLVDSGEKEKAYQOMLEG 642				Db	1529 KNI7SAADKTITWIS-LGRLRILTQGHSASVWNLSLSDGQTLASTSOBTIKWNLN 1587
220 --IEEAKDRRLTILMKRKHPRASLILDDWDWVSLWKAFCDSQCCILT-----TRDK--- 267				Qy	1116 LLLPLHLERGHNGCYTCRCSAFSVDSTLALGDDNGEIRINWVNSGELLHLICAPLSEGAAAT 1175
643 MLYQGAGQFVHWLHHRPRMPPWVILQDFBELLTLAASESDQRFLDTVTGALBELSPDKEKL 702				Db	1588 GEL-TYTURGHSDVYVYULSFSPDGKTIASASDDGTWIKLWNVNGTLK-----TFQG---
268 --SVTDVUMGPCKVNPVPESSLGKEKGL---EILSLFNM-KKKADL---PEQHNS 312				Qy	1176 HGGIVTVTDLCFSPDGSRMNLSAGGY--IKWNVN 1204
703 IYTLRADFIAPCLEIPTLAKLQIQQSSSTLPPCILTOSEYRRLTHPAEKVGLTVDPPEVE 762				Db	1639 HRGGYRVSVSFSPDGKILAS-GGHDITTVKWNL 1669
313 IIEKCKGSPLVLSLIGAILRDPENRWEY-----YLKQLOLONKQFKRIRKSSY 359				RESULT 14	
763 LQELQNLSPGDPFLLEFLQEP---WEYTRDKGVTILQYQYLQIGGK---ALEKAAQG 815				YI24 ANASP ID: YI24_ANASP STANDARD; PRT; 1683 AA.	
360 DYEALD-EAMS-----ISVEMLRED-----IKEYYDTLSILQOKDVVKPTK 398				AC Q8YV57; AC Q8YV57;	
816 YVTDLDSAAQECTRWIIFSLTOLGEGTBDTRRVLKSLIVKRY---PVALVERTLQVLT 873				DT 28-FEB-2003 (Ref. 41, Created)	
399 VCLWLMDETEE-----VEDLQ-----EFVNLWLFCDRNKSFYKYLH 438				DT 28-FEB-2003 (Ref. 41, Last sequence update)	
874 AKLVVNGGEWGRGKRQGAGGRQGENILITTPSUTTEVAEVITL-----RYWSTLKWVL- 929				DT 05-JUL-2004 (Ref. 44, Last annotation update)	
439 DLQVDFLTEKNCSQLQDLHKLKITQFORYHOPHTLSPD----QEDCM 481				DB Hypothetical WD-repeat protein all12124.	
930 -----EENPSRLS-HRD-IEQSALWQMQNQDFFLQGVLRLAEETYLNITDEL 979				GN Ordered locust names-all12124.	
482 YH--YNFL---AYTHMASAKMHKELCALMFSLWIKAKTEL---VGPAHLIHFVEYRHL 533				OS Anaebana sp. (strain PCC 7120).	
980 SWDVQHPIEACILHERRKQDOSRQRAORAVSIISTLGLTAFGLAVAYQQTQNAQLK 1039				OC Cyanobacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.	
534 DKDC-AVSEN-----QEPFLSNGHLLGRQPPIVQGL---CEPTESETVQAKOAK 585				NCBI_TaxID: 103690; NCBI_TaxID: 103690;	
1040 BTOALNSLSENFLSHQOLEALMTSYQAGKEVONI-SLGIPIPDTRTQATLQLQAVNTQ 1098				RN SEQUENCE FROM N.A.	
586 QEVUDNGMLYLEWINKNKNITNLSRLVRPHTDAYHGFSEGDORIAASCDAKTLQVEKAE 645				RP RP	
1099 ER--NTRILNNAW-----VTSV-----YSPDSEVIASGSVNTLTHWRRD 1136				RP MEDLINE:21595285; PubMed:11759840;	
646 TGEKLEIKAHEDDEVLLCAFPSTDDRFLATCSDYDVKVWIKWNTGELVHTYDEHSEQVNCC 705				RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Watanabe A., Iriuchi M., Ishikawa K., Kimura T., RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakazaki N., Shimpou S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S.,	
1137 -GKLLTGTGNDGYNVSFSPDGEILASASADSTKILW-ORNLGHDQGKTSV 1194				RA "Complete genomic sequence of the filamentous cyanobacterium Anabaena sp. strain PCC 7120.", DNA Res. 8:205-213 (2001).	
706 HPTNSHHLIATGSSDCFLKWDLNKRECHNTMFGTINSVHCRFSPDDJLASSADG 765				CC CC	
1195 SFSPNGE-IIASGSDHTINWNSRAGK-LIISLNLHGQSQVNISIKSPSEGDTIASDDG 1251				CC CC	
766 TFLKLWDATSAERKSINVKOFFPLNLDKRECHNTMFGTINSVHCRFSPDDJLASSADG 824				CC CC	
1252 TIRLW-----SLGDRPLITI-----PSHTKQVL-----AVTFSPDGTQIVSAGADNTYKWL 1297				CC CC	

DR	PROSITE; PS50294; WD_REPEATS_REGION; 1.	Repetitive protein; Repeat; WD repeat.	Qy	777 ERKSINVQFLNEDQEDMEVIVKCCSWWSADGARIMVAANKNLFLFDIHTSGLLGEIH 836	Db	1231 LLKTFLNGHQDWYNTTSDSPDGKTLIASADKTKLWRLAGKLVYKL 1277
KW	Complete proteome;					
FT	REPEAT 1070 1109	WD 1.				
FT	REPEAT 1111 1150	WD 2.				
FT	REPEAT 1153 1192	WD 3.				
FT	REPEAT 1195 1236	WD 4.				
FT	REPEAT 1280 1318	WD 5.				
FT	REPEAT 1320 1359	WD 6.				
FT	REPEAT 1361 1400	WD 7.				
FT	REPEAT 1402 1441	WD 8.				
FT	REPEAT 1444 1483	WD 9.				
FT	REPEAT 1486 1525	WD 10.				
FT	REPEAT 1528 1567	WD 11.				
FT	REPEAT 1570 1609	WD 12.				
FT	REPEAT 1611 1650	WD 13.				
SQ	SEQUENCE 1683 AA; 185459 MW; F7CB3611F54F137 CRC64;					
Qy	Query Match 10:2%; Score 672; DB 1; Length 1683;		Qy	1009 IQFTADBTLLSSDPAEIVWWQLDKCIF--LRGHQETVVKDPLRUKNSRL-SWSFD 1064	Db	1452 VNFSPDGKTLIASASRNTVYKLWVNSDGR--FCKLTGLKHTDEVWVFSFSPDGKTLIASASD 1509
Matches 201; Conservative 198; Pred. No. 5..1e-30; Mismatches 490; Indels 244; Gaps 41;			Qy	1065 GTVKVWNLTENKEKFVUHQGTVLSCDISHATKESSTADTKATKIVSFPLLPHEL 1123	Db	1510 KTRLWDGSFLNLKSLPAHNDLVSYAENPNPGMSMLASTADTKVTKLVRSHDHL-LHTEF 1568
Qy	95 SSSSGKOSVGTSITSYRTVTCGUVPPDPVWVTRKLVNIAQQKLISKURKGPGWTING 154		Qy	1124 RGHINGYTCRCSAFSVDSVSTLIALGDGNGBIRIWVNSGELFLCPLSEGAATHGGWVTDL 1183	Db	1569 SGHSNVVVYSSSFSPDORYIASASEDTKVKIRDG---HLILTPQ---HQAGQMSA 1619
Db	553 ASGGKSS--WVQAGRIPQ--LROGRHIPSNEQWIKTIR-PGVNPLEA 596		Qy	1184 CFSPDGKMLIS 1194	Db	1620 IFSPDGKTLIS 1630
Qy	156 MAGCGKSVLAAEAVRDHSLSLEGCP---PG3YHWVSVGKDKDSGLM---KLQNUCTRL 206					
Db	597 LAR---KLGEGWGETHLLTEGMHLHQVGFYWLRSLPOQTVLVIDQFELTIAPTP 651					
Qy	207 DQDEFSQRQLPLNIEFAKDRILRMLRKHPSRLLDDWVSKAFDSQCQILITR'D 266					
Db	652 DR-ELEFLELLGAVQYAGDRFLKLI-----TIRA----- 679					
Qy	267 KSVTDSVMPGVKVVPESSIGKEGLEILSLEVNNMKKAQDLPQEHSITKECK--GSPLVV 324					
Db	680 -----DFTAPCLEVALREALQVASYLV--PKLSSLIDYERVILHPAQOQVQVEA 728					
Qy	325 SLIGALLR-----DFPNRWEYTLKQLOQNQPKKRKSSSYD----- 360					
Db	729 ELYBVLRELAQSVGPBP-LELFVPLQWQTAGKLQSYOFQLGIGKGLERSCQGV 787					
Qy	361 YEALDEAMS-----ISVEMLRDIDK-----YTDL-----STILOKDVKVPTKVL 401					
Db	798 YESLUPPQLQECAKWIFPLSLTGEGTEPTRRIYSDSLIVKTYPAGLVEQTINVLTNKL 847					
Qy	402 ILWDMETBEVDILOFVNRSLSLFCDRNKSQDQDILHKII 461					
Db	848 VVNLNEA-----IEAQGKSFSPTPNPLSTPFVTEVAHEILIRHWSLT 891					
Qy	462 TQFRYHQPHLSPQ--EDCMWY-----NFLAYMHSAGKHKCALMSELDWIK 513					
Db	892 RWLLENRDRURKQOQINHAQWQSGSKQADF---LOGARLAEADPYTWDELGAD 948					
Qy	514 T-BLVGP-----AHLIHFVEYRHILDEKOCAV-----SENFOQEFL 548					
Db	949 VQFIGACLAERKHOQKANRUKQADRAVALSVGIAVASFGLAGLWQGREAOFEIA 1008					
Qy	549 SLN----GHILLGROFPNTPVQLGICCEPSTSYIQQKLQKNGMYLWINKNKT 604					
Db	1009 ALNSSSQANLISHHQLAAL-----ASLRKAQHVYTAVPNPNLKLATV 1053					
Qy	605 NISRLV-----VRPHTDAYTAHCASESDQRIASGADTQVKAETGKLEIAH 656					
Db	1054 TLUQALPEMQRERNLQEGHKDGVVISISRDRQTIASGSLDQTKLWRSD-GRLFRTLNGH 1112					
Qy	657 EDEVLCCAFSTDDRFIATCSVDEKKVWNSNTGELYHTEDEHSEQVNCCCHPTNSHHLLL 716					
Db	1113 EDAVSVSFSPDGQFIASGSDKXKLUWQTSDFGTLKTTGHEQTVNNVYFSPDGKN--L 1170					
Qy	717 ASASSDHSIKWMDTSGQMLMTLGHSGAVTVRFSFDGOTIAAGSDKTVKLWHRQDGK 1230					
Db	1171 ASASSDHSIKWMDTSGQMLMTLGHSGAVTVRFSFDGOTIAAGSDKTVKLWHRQDGK 1230					
Qy	Query Match Best Local Similarity	10.1%; Score 666; DB 2; Length 1193;	Qy	1193 AA; 130908 MW; 07AB8750D470E6C3 CRC64;	Db	Pred. No. 6.9e-30;



Copyright (c) 1993 - 2005 Compugen Ltd.	GenCore version 5.1.6	Abg65660 Mouse apo		
OM protein - protein search, using sw mode1	Search time 176 Seconds	Abg13410 Novel hum		
Run on: January 27, 2005, 18:25:54 ; Search time 176 Seconds (without alignments)	2543.717 Million cell updates/sec	Aay97648 Apaf-1 pr		
Title: US-10-646-396-2		Abj04764 Apaf-1 pr		
Perfect score: 6619		Abb81757 Tumour ne		
Sequence: 1 MDAKARNCLLQHREALEKD1 EKTYVTVNDNLGILYIQLTLE 1248		Abj04761 Apaf-1 pr		
Scoring table: BL0SUM62		Aaw55885 Rat telom		
Gapext 0.5		Add21418 Rat TERT		
Searched: 2002273 seqs, 358729299 residues		Add21417 Rat TERT		
Total number of hits satisfying chosen parameters:	2002273	Add21424 Mouse TER		
Minimum DB seq length: 0		AAw61348 Mouse tel		
Maximum DB seq length: 2000000000		Aad63119 Rat Prote		
Post-processing: Minimum Match 0*	Maximum Match 100%	AAw61321 Human Pro		
Listing first 45 summaries		Aaw61347 Human tel		
Database :	A_Geneseq_22Sep04:*	Adk40934 Novel hum		
	1: _geneseqp1980s:*	Aaw55887 Human tel		
	2: _geneseqp1990s:*			
	3: _geneseqp2000s:*			
	4: _geneseqp2001s:*			
	5: _geneseqp2002s:*			
	6: _geneseqp2003s:*			
	7: _geneseqp2003bs:*			
	8: _geneseqp2004s:*			
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.				
SUMMARIES				
Result No.	Score	Query Match Length DB ID	Description	
-	-	-	-	
1	6619	100.0	1248 4 AAY97636	Aay97636 Apaf-1XL
2	6619	100.0	1248 5 ABG65661	Abg55661 Human apo
3	6619	100.0	1248 6 ABP72163	Abp72163 Human APA
4	6616	100.0	1248 4 AAY97646	Aay97646 Apaf-1XL-
5	6616	100.0	1248 4 AAY97639	Aay97639 Apaf-1XL-
6	6616	100.0	1248 4 AAY97643	Aay97643 Apaf-1XL-
7	6615	99.9	1248 4 AAY97644	Aay97644 Apaf-1XL-
8	6614	99.9	1248 4 AAY97645	Aay97645 Apaf-1XL-
9	6614	99.9	1248 4 AAY97641	Aay97641 Apaf-1XL-
10	6613	99.9	1248 4 AAY97647	Aay97647 Apaf-1XL-
11	6611	99.9	1248 4 AAY97642	Aay97642 Apaf-1XL-
12	6548.5	98.9	1237 4 AAY97638	Aay97638 Apaf-1WD
13	6548.5	98.9	1237 7 ADP65108	Adp65108 Human apo
14	6352.5	96.0	1205 2 AAW91072	Aaw91072 Apoptosis
15	6352.5	96.0	1205 4 AAY97637	Aay97637 Apaf-1L_P
16	6282	94.9	1194 2 AAW91071	Aaw91071 Apoptosis
17	6282	94.9	1194 3 AAY4932	Aay4932 Human ful
18	6282	94.9	1194 4 AAY97649	Aay97649 Wild type
19	6282	94.9	1194 6 ABB82741	Abg5662 Human apo
20	6282	94.9	1194 7 ADP65303	Adp65303 Human apo
21	6282	94.9	1194 7 ADP65303	Adp65303 Human apo
22	6282	94.9	1194 8 ADG87139	Adg87139 Human Apa
23	6112	92.3	1149 4 AAY97640	Aay97640 Apaf-1XL
24	6003.5	90.7	1199 8 ADM87180	Adm87180 Human pro
25	5933.5	89.6	1526 8 ADM87179	Adm87179 Human pro
			ALIGNMENTS	
			RESULT 1	
			ID AAY97636 standard; protein; 1248 AA.	
			XX	
			AC AAY97636;	
			XX	
			DT 20-APR-2001 (first entry)	
			XX	
			DE Apaf-1XL protein sequence.	
			XX	
			KW Apaf1; CBD-4 homologue; cytochrome c-dependent activation; caspase-3; apoptosis signalling pathway; cancer; autoimmune disease; variant; hereditary disease; Apaf-1XL.	
			XX	
			KW Homo sapiens.	
			XX	
			PN WO20100827-A1.	
			XX	
			PD 04-JAN-2001.	
			XX	
			PP 30-JUN-2000; 2000WO-US018039.	
			XX	
			PR 30-JUN-1999; 99US0-0141718P.	
			XX	
			PA (UNMI) UNIV MICHIGAN.	
			XX	
			PI Nunez G, Hu Y;	
			XX	
			DR WPI; 2001-112454/12.	
			DR N-PDB; AAA91115.	
			XX	
			PT Compositions for screening apoptosis pathway agonists and antagonists, useful for the treatment and diagnosis of cancer and autoimmune diseases, comprises new splice variants of wild-type Apaf-1 gene.	
			XX	
			CC Disclosure; Fig 25; 101pp; English.	
			CC This sequence represents an Apaf-1 variant of the invention. The variants of the invention are all splice variants of a wild-type Apaf-1 gene (a mammalian homolog of CEB-4 that participates in cytochrome C-dependent activation of caspase-3). The DNA is useful in screening assays for identifying apoptosis pathway (ant)agonist, which are in turn useful as potential therapeutic and diagnostic or prognostic tools for diverse types of cancers, autoimmune diseases and hereditary diseases and for screening compounds that modulates the interaction of Apaf-1 with other members of the signalling pathway i.e. their substrates or ligands. The protein encoded by the Apaf-1 variant genes are useful in a cell-free assay system and the antibody generated to the translation	

CC product are used in immunoprecipitation assays to isolate new Apaf-1 pathway constituents or their natural mutants	Qy 961 BAQVSCCUSPHLQYIAFGDENGALIBELVNNRIFQSRFQHKKTVWHIOFTADEKTLIS 1020
Sequence 1248 AA;	Db 961 EAQVSCCUSPHLQYIAFGDENGALIBELVNNRIFQSRFQHKKTVWHIOFTADEKTLIS 1020
Best Local Similarity 100.0%; Score 661.9; DB 4; Length 1248;	Qy 1021 SSDDAEIQWNNMOLDKCIFLKGHQETVKDFRLKNSRLLSWFDGTWKVNITGNKEKD 1080
Matches 1248; Conservative 0; Pred. No 0; Mismatches 0; Indels 0; Gaps 0;	Db 1021 SSDDAEIQWNNMOLDKCIFLKGHQETVKDFRLKNSRLLSWFDGTWKVNITGNKEKD 1080
Qy 1 MDAKARNCLQHREALKDIKTYSYIMDIHMSDGFLTSEEKVRNVEPTOCQRAMLKMI 60	Qy 1081 FVCHQGTVLSCDISHDATKFESTSADTKAKWFDLILPLHLRGNGCVRCSAFSDST 1140
Db 1 MDAKARNCLQHREALKDIKTYSYIMDIHMSDGFLTSEEKVRNVEPTOCQRAMLKMI 60	Db 1081 FVCHQGTVLSCDISHDATKFESTSADTKAKWFDLILPLHLRGNGCVRCSAFSDST 1140
Qy 61 LKKNDTSVSPNALIHEGYKDALLHDQIPVSSSGRSVSGLTSTVTRVLCBEGVP 120	Qy 1141 LLAYGDDNGEIRIWNWSNGELHLHCAPISEGAATHGSGWVTDLCFSPDGMLIAGGTYK 1200
Db 61 LKKNDTSVSPNALIHEGYKDALLHDQIPVSSSGRSVSGLTSTVTRVLCBEGVP 120	Db 1141 LLAYGDDNGEIRIWNWSNGELHLHCAPISEGAATHGSGWVTDLCFSPDGMLIAGGTYK 1200
Qy 121 QRPVVFVTRKLUNAQKQLSKLGEPGVNTIHGMACGCCSVTAEAEDVHSILEGGPG 180	Qy 1201 WNWVVTGESSQPFYTNTNLKXHIVSPDKTKTTVDNLGLYIQLQE 1248
Db 121 QRPVVFVTRKLUNAQKQLSKLGEPGVNTIHGMACGCCSVTAEAEDVHSILEGGPG 180	Db 1201 WNWVVTGESSQPFYTNTNLKXHIVSPDKTKTTVDNLGLYIQLQE 1248
Qy 181 GVRVSVSVERQDKESGLKLMKLNQNLTRLDQDSFSQRQLPLNTEAKDRRLMLRKHPRSSL 240	RESULT 2
Db 181 GHVWVSVKQDKSGLLMKLNQNLTRLDQDSFSQRQLPLNTEAKDRRLMLRKHPRSSL 240	ABG65661 standard; protein; 1248 AA.
Qy 241 LDGVWDWSWVLAKFDSQCQLLTTRDKSYTDSMGPKXXVVESSLGKGBLISLFVN 300	ID ABG65661;
Db 241 LDGVWDWSWVLAKFDSQCQLLTTRDKSYTDSMGPKXXVVESSLGKGBLISLFVN 300	XX
Qy 301 MKRADLPQASIIKECKGSPLVNSLIGALIDPFRNWEYLKOLQNKQFRKRSYYD 360	XX Human apoptotic protease activating factor 1 (Apaf-1) exon 1 3' end.
Db 301 MKRADLPQASIIKECKGSPLVNSLIGALIDPFRNWEYLKOLQNKQFRKRSYYD 360	XX Antisense compound; apoptotic protease activating factor 1; Apaf-1;
Qy 361 YEALDEAMISYSTEMREDIDKTYDTDSLTLQDKYKVPUKVLIDMDMETEEVDILQEFVN 420	XX colon cancer; breast cancer; haemopoietic cancer; prostate cancer; antisense gene therapy; infection; inflammation; tumour formation; antisense technology.
Db 361 YEALDEAMISYSTEMREDIDKTYDTDSLTLQDKYKVPUKVLIDMDMETEEVDILQEFVN 420	XX Homo sapiens.
Qy 421 KSLIFCDRNGKSFRYLDHQDQLTETRNCSQODLHKITQFRYQPHLSPQEDC 480	XX
Db 421 KSLIFCDRNGKSFRYLDHQDQLTETRNCSQODLHKITQFRYQPHLSPQEDC 480	XX
Qy 481 MYYNFLAYHMASAROHKCALMFSLWIKAKTVELYGPALHILIEFPYRHILDEKCAV 540	XX
Db 481 MYYNFLAYHMASAROHKCALMFSLWIKAKTVELYGPALHILIEFPYRHILDEKCAV 540	XX
Qy 541 SENFOEFLSLNGLLGRGPNTVOLGLCEPETSEVYQQAKLQAKQEVVDNGMLYLEWINK 600	XX
Db 541 SENFOEFLSLNGLLGRGPNTVOLGLCEPETSEVYQQAKLQAKQEVVDNGMLYLEWINK 600	XX
Qy 601 KNITNLSLRVYRPHTDAAVHACFEDGRIASCQADKTLQYKAEKGKLLJIKAHEDEV 660	XX
Db 601 KNITNLSLRVYRPHTDAAVHACFEDGRIASCQADKTLQYKAEKGKLLJIKAHEDEV 660	XX
Qy 661 LCCAFSTDPRRTATSYDKVKCWNSMTGELVHTDEHSQVNCHFTNSHHLLATGS 720	XX Novel antisense compound that hybridizes and inhibits nucleic acid
Db 661 LCCAFSTDPRRTATSYDKVKCWNSMTGELVHTDEHSQVNCHFTNSHHLLATGS 720	XX encoding apoptotic protease activating factor 1, for treating hyperproliferative disorder e.g. cancer, preferably breast, colon, or prostate cancer.
Qy 721 SDCFLKLWDLNQKECRNTMFGHTNSVNHCFSPPDDKLASSADGTLKWDTSANERKS 780	XX Disclosure; Page 10-114; 138pp; English.
Db 721 SDCFLKLWDLNQKECRNTMFGHTNSVNHCFSPPDDKLASSADGTLKWDTSANERKS 780	XX DR 2002-45330349.
Qy 781 INYKQFFNLNDPQDMETVVKCCSWSDGARIMTAAKKIFIDITSGLAGEHTGH 840	XX DR N-PSDB; ABK35570.
Db 781 INYKQFFNLNDPQDMETVVKCCSWSDGARIMTAAKKIFIDITSGLAGEHTGH 840	XX
Qy 841 SPOYCDSPONHLAVALSQCYVELWNTDERSKYADCGHFLSWVHGGMFSGDGSSFLTS 900	XX PT PT PT PT
Db 841 SPOYCDSPONHLAVALSQCYVELWNTDERSKYADCGHFLSWVHGGMFSGDGSSFLTS 900	XX where the disease or condition is a hyperproliferative disorder such as cancer, preferably breast, colon, haemopoietic or prostate cancer. It is also useful for diagnostics, therapeutics, prophylaxis, as research reagents and kits, for distinguishing functions of various members of a biological pathway, and in antisense gene therapy. (I) is also useful prophylactically, e.g. to prevent or delay infection, inflammation or
Qy 901 SDQQTIRLWETKVKCKNSAVMLKOEIDVUEGENEMYLAVDHRRQLQINGTQDYL 960	XX
Db 901 SDQQTIRLWETKVKCKNSAVMLKOEIDVUEGENEMYLAVDHRRQLQINGTQDYL 960	XX

tumour formation. This is the amino acid sequence of an Apaf-1 protein CC DNA encoding which used in the creation of antisense Oligonucleotides for CC modulating the activity and expression of Apaf-1.

XX	Sequence 1248 AA;	Qy	961 BAQVSCCCLSPHQYIAFGDENGAIIBILEVNNRIFOSRQHKKTYWHIQPTADEKLIS 1020
SQ		Db	961 BAQVSCCCLSPHQYIAFGDENGAIIBILEVNNRIFOSRQHKKTYWHIQPTADEKLIS 1020
Query Match 100.0%; Score 6619; DB 5; Length 1248;		Qy	961 BAQVSCCCLSPHQYIAFGDENGAIIBILEVNNRIFOSRQHKKTYWHIQPTADEKLIS 1020
Best Local Similarity 100.0%; Pred. No. 0;		Db	1021 SDDDAIQLQWNLQDKCIFLRHQETVKDFULLPSLSSMSFDGTVKVNNTITGNKEKD 1080
Matches 1248; Conservative 0; Mismatches 0; Gaps 0;		Qy	1021 FVCHQCTVLSPSDISHDATEFISTSADKTAKWSFDLPLPBLRQINGCVRCSAFSVDST 1140
1 MDAKARNCLLQHREALERDKIKTSYIMDHMISDGFLTISEEEVKVRNEPTQQOGRAMLKMI 60		Db	1021 FVCHQCTVLSPSDISHDATEFISTSADKTAKWSFDLPLPBLRQINGCVRCSAFSVDST 1140
1 MDAKARNCLLQHREALERDKIKTSYIMDHMISDGFLTISEEEVKVRNEPTQQOGRAMLKMI 60		Qy	1141 LLATGDDNGEGRIMVNSNGELHLHCAPLSESEGAAHTGGWTDLCSPDGMKMLISAGGYIK 1200
61 LKKNDNSVSYSTNALHEGYKDLAALHHGIPVYSSSSGKDSVSGSTSRTTVLCEGGVP 120		Db	1141 LLATGDDNGEGRIMVNSNGELHLHCAPLSESEGAAHTGGWTDLCSPDGMKMLISAGGYIK 1200
61 LKKNDNSVSYSTNALHEGYKDLAALHHGIPVYSSSSGKDSVSGSTSRTTVLCEGGVP 120		Qy	1201 WNWVTGESESSQTFTYNTGTLKXHYSPDFKTYVTDNLGILYLQTLLE 1248
Qy	121 QRPVVETRKLVNAIQQKLSKLKGPGWTTIHMAGCGKSVLAAEAVRDLSLEGCPFG 180	Db	1201 WNWVTGESESSQTFTYNTGTLKXHYSPDFKTYVTDNLGILYLQTLLE 1248
Db	121 QRPVVETRKLVNAIQQKLSKLKGPGWTTIHMAGCGKSVLAAEAVRDLSLEGCPFG 180		
Qy	181 GVHWYSGKDKSGLMLQNLCLTRLDQDESFSQRPLNTEAKDRLRLLRKHPRSLI 240		RESULT 3
Db	181 GVHWYSGKDKSGLMLQNLCLTRLDQDESFSQRPLNTEAKDRLRLLRKHPRSLI 240	Db	ABP72163 standard; protein; 1248 AA.
Qy	241 ILLDDWDSWVLKAQFDSQCOLLITTRDKSTDSVMPKTYVPESSLGKCKGLEILSLFVN 300	Db	ABP72163 ;
Db	241 ILLDDWDSWVLKAQFDSQCOLLITTRDKSTDSVMPKTYVPESSLGKCKGLEILSLFVN 300	XX	XX
Qy	301 MKKADLPPEQHSIIKECKGSPLVVSIIQKLLRDPFRWETYLKQLOQNPKPRKSSYD 360	Db	ABP72163 ;
Db	301 MKKADLPPEQHSIIKECKGSPLVVSIIQKLLRDPFRWETYLKQLOQNPKPRKSSYD 360	XX	DT 22 - APR - 2003 (first entry)
Qy	361 YEALDEAMTSIVEMLRDIDKYYTDLISLQDKVYKPTKVLCILWDMETEEVEDILQEFTVN 420	Db	XX Human APAF1, inducer of cell death.
Db	361 YEALDEAMTSIVEMLRDIDKYYTDLISLQDKVYKPTKVLCILWDMETEEVEDILQEFTVN 420	XX	XX Human; APAF1; cell death; apoptosis; neurodegenerative disease; heart disease; cardiomyopathy; cardiant; neuroprotective; gene therapy; gene; ss.
Qy	421 KSLIFCDRNGKSPRYVTHLQDVFETKNCQSOLQDLHKKLTITOPRYHQPHTLSPDQEDC 480	Db	XX Homo sapiens.
Db	421 KSLIFCDRNGKSPRYVTHLQDVFETKNCQSOLQDLHKKLTITOPRYHQPHTLSPDQEDC 480	XX	XX WO2003004606-A2.
Qy	481 MYWINFLAYMASAKNHKELCALMSLDWKAKTELGVPAHLHBEPEVYHILDEKDCAV 540	Db	XX 16 - JAN - 2003 .
Db	481 MYWINFLAYMASAKNHKELCALMSLDWKAKTELGVPAHLHBEPEVYHILDEKDCAV 540	XX	XX PD
Qy	541 SENFOEFLSNGHLLGRQPFENIVOLGLCCEPETSEVYQDAKQEVQDNGMLYLEWINK 600	Db	XX 03 - JUL - 2002 ; 2002WO-US021002 .
Db	541 SENFOEFLSNGHLLGRQPFENIVOLGLCCEPETSEVYQDAKQEVQDNGMLYLEWINK 600	XX	XX PR
Qy	601 KNITNLSLRYTPRHDAYACPFSDGORIASCGADKTLQVKARTGEKLEIKAHEDY 660	Db	XX 03 - JUL - 2001 ; 2001US - 00888158 .
Db	601 KNITNLSLRYTPRHDAYACPFSDGORIASCGADKTLQVKARTGEKLEIKAHEDY 660	XX	XX PA (UYCO) UNIV COLUMBIA NEW YORK .
Qy	661 LCCAFSTDREPIATCSVDKCVTKWNSMTGELVHTYDEHSQVNCCHFTNSHILLATGS 720	Db	XX PI Troy CM, Shelanski ML;
Db	661 LCCAFSTDREPIATCSVDKCVTKWNSMTGELVHTYDEHSQVNCCHFTNSHILLATGS 720	XX	XX DR WPI ; 2003 - 21051 / 20 .
Qy	721 SDCEFLKLWDLNQKECRNTMFGHTNSYNHCRSPDDKLASASDGTKLWMDATSAERCS 780	Db	XX DR N - PDB ; ABZ58107 .
Db	721 SDCEFLKLWDLNQKECRNTMFGHTNSYNHCRSPDDKLASASDGTKLWMDATSAERCS 780	XX	XX PT New nucleic acid encoding an inhibitor-of-apoptosis protein, useful for treating cancer, neurodegenerative disorder or cardiomypathy.
Qy	781 INVQFFPLIEDPOEDMEVYKCCSWASDARIMTAAKKIELFDIHTSGLGETHTGH 840	Db	XX PS Disclosure; Fig 21A; 12app; English.
Db	781 INVQFFPLIEDPOEDMEVYKCCSWASDARIMTAAKKIELFDIHTSGLGETHTGH 840	XX	XX CC The present sequence is the protein sequence for human APAF1, a protein CC that induces cell death. The invention provides a nucleic acid, such as CC an antisense oligonucleotide, which specifically hybridises to a nucleic CC acid encoding a protein that induces cell death, especially APAF1, RAIDD CC or Diablo/SMAC. A claimed method for inhibiting a cell's death CC (especially a neuronal cell's death) comprises contacting the cell with CC the nucleic acid under conditions permitting the nucleic acid to enter CC the cell, especially the use of a vector, liposome, or electrical or CC electrical means. The method is used to treat a neurodegenerative CC disorder, especially a brain disorder or central nervous system disorder, CC or a heart disorder, especially cardiomypathy, in a human (all claimed) CC Sequence 1248 AA;
Qy	901 SDDOTIRLWETKVKCKNSAVALMKQEVYDVFOENEVMVLAHDHRRQLINGRTGQIDYL 960	Db	XX SQ
Db	901 SDDOTIRLWETKVKCKNSAVALMKQEVYDVFOENEVMVLAHDHRRQLINGRTGQIDYL 960	XX	XX Query Match 100.0%; Score 6619; DB 6; Length 1248;
Qy	901 SDDOTIRLWETKVKCKNSAVALMKQEVYDVFOENEVMVLAHDHRRQLINGRTGQIDYL 960	Db	XX

Best Local Similarity	100.0%	Pred. No.	0;
Conservative	0;	Mismatches	0;
Matches	1248;		
Y			
b			
1 MDAKRNCLQHQRALEKDIKTYSIMDMSICFELTISEBEKVREHPTQQRAMLKKMI	60	Db	Db
1 MDAKRNCLQHQRALEKDIKTYSIMDMSICFELTISEBEKVREHPTQQRAMLKKMI	60	Qy	Qy
61 LRDNDSYSPSYTNAALLHEGKDLAALHGDPVVSSSGKDSVSGITSVRTVLCEGGVP	120	Db	Db
61 LRDNDSYSPSYTNAALLHEGKDLAALHGDPVVSSSGKDSVSGITSVRTVLCEGGVP	120	Qy	Qy
121 QRPVVFTTRKLVNAIQQLSLKKGEBPOWWTGHAGGCKSVLAEARDSHSLEGFPF	180	Db	Db
121 QRPVVFTTRKLVNAIQQLSLKKGEBPOWWTGHAGGCKSVLAEARDSHSLEGFPF	180	Qy	Qy
181 GYHWSVGDKDSGKSLMQLONLCTRLDODESFSQRLPLNTEAKDRFLRILMKHPRSLI	240	Db	Db
181 GYHWSVGDKDSGKSLMQLONLCTRLDODESFSQRLPLNTEAKDRFLRILMKHPRSLI	240	Qy	Qy
241 ILLDWDWSWLKAPEQSOCQILLIITRDKSVDTSVMGKYYVPPVESSLGKEKGKLGELISIFVN	300	Db	Db
241 ILLDWDWSWLKAPEQSOCQILLIITRDKSVDTSVMGKYYVPPVESSLGKEKGKLGELISIFVN	300	Qy	Qy
301 MKRADLPEQHSIKECKCSPLVSSLCALLRDPTRWETYLKOLQNKQFRKRKSSYD	360	Db	Db
301 MKRADLPEQHSIKECKCSPLVSSLCALLRDPTRWETYLKOLQNKQFRKRKSSYD	360	Qy	Qy
361 YEALDEAMASIVENLREDKDYTDLSLQDVKYTKVCLIDMTEMEEVDILEDFVN	420	Db	Db
361 YEALDEAMASIVENLREDKDYTDLSLQDVKYTKVCLIDMTEMEEVDILEDFVN	420	Qy	Qy
421 KSLLFLCDRKNKSFYFLHDQLQDFLTENKNSQLDLHKLKITQFRYQPHTLSPQEDC	480	Db	Db
421 KSLLFLCDRKNKSFYFLHDQLQDFLTENKNSQLDLHKLKITQFRYQPHTLSPQEDC	480	Qy	Qy
481 MYWYNFLATHMASKQHKELCALMFSLWDIWAKTLEVPAHLTHEFVYRHLIDEDKCAV	540	Db	Db
481 MYWYNFLATHMASKQHKELCALMFSLWDIWAKTLEVPAHLTHEFVYRHLIDEDKCAV	540	Qy	Qy
541 SENFOEFLSLNGLHIGROFPNVQGLCEPETSSEVYQAKLQAKQEVYDNGMLYLEWINK	600	Db	Db
541 SENFOEFLSLNGLHIGROFPNVQGLCEPETSSEVYQAKLQAKQEVYDNGMLYLEWINK	600	Qy	Qy
601 KNTNTNLSRLYVRPHFTDAYHAFCSEDQQTASCAGADTKLQVFAETGEKJLKIAHEDEV	660	Db	Db
601 KNTNTNLSRLYVRPHFTDAYHAFCSEDQQTASCAGADTKLQVFAETGEKJLKIAHEDEV	660	Qy	Qy
661 LCCATSDDRFIATCSVDKKVLWNLQKCRNTMFMEHTNSYHCRSPDPDKLASSADGTKLWMDATSANBRKS	720	Db	Db
661 LCCATSDDRFIATCSVDKKVLWNLQKCRNTMFMEHTNSYHCRSPDPDKLASSADGTKLWMDATSANBRKS	720	Qy	Qy
721 SDCEFLKLWNLWNLQKCRNTMFMEHTNSYHCRSPDPDKLASSADGTKLWMDATSANBRKS	780	Db	Db
721 SDCEFLKLWNLWNLQKCRNTMFMEHTNSYHCRSPDPDKLASSADGTKLWMDATSANBRKS	780	Qy	Qy
781 INVKOFFNLEDPEDMEVIVKCCWSADGARIMVAKKKK1FLFDIHTSGLGEITHGHH	840	Db	Db
781 INVKOFFNLEDPEDMEVIVKCCWSADGARIMVAKKKK1FLFDIHTSGLGEITHGHH	840	Qy	Qy
841 STIVQYCDFSQNHAVAVSQCVEWNTDSRSKVADECRGHLSSWQGMFSPDGSSFLTS	900	Db	Db
841 STIVQYCDFSQNHAVAVSQCVEWNTDSRSKVADECRGHLSSWQGMFSPDGSSFLTS	900	Qy	Qy
901 SDDPDTIRLNETKCKCSNAMSMLQEVYDVFOENEMMLAVDHARRLQINGERTQDYLIT	960	Db	Db
901 SDDPDTIRLNETKCKCSNAMSMLQEVYDVFOENEMMLAVDHARRLQINGERTQDYLIT	960	Qy	Qy
961 EAQVSCCCUSPHLCYIAGFDENGIAIRLLEAVNNRIFOSRFHKKTHPHIOFTAETKLIS	1020	Db	Db
961 EAQVSCCCUSPHLCYIAGFDENGIAIRLLEAVNNRIFOSRFHKKTHPHIOFTAETKLIS	1020	Qy	Qy
1021 SSDDAEIQWNWQDJKC1FLRQHQTIVKDFRLLNSRLLWSDFGTYKWN1ITGNKBD	1080	Db	Db
1021 SSDDAEIQWNWQDJKC1FLRQHQTIVKDFRLLNSRLLWSDFGTYKWN1ITGNKBD	1080	Qy	Qy
RESULT 4			
AAV97616			
1D AAY97646 standard; protein; 1248 AA.			
XX AAY97646;			
AC AAY97646;			
DT 20-APR-2001 (first entry)			
XX Araf-1XL-K160R protein sequence.			
XX Araf-1; CED-4 homologue, cytochrome c-dependent activation; caspase-3; apoptosis signalling pathway; cancer; autoimmune disease; variant; hereditary disease; Araf-1XL-K160R.			
KW apoptosis			
KW homologue			
KW cytochrome c-dependent activation			
KW caspase-3			
KW autoimmune disease			
KW hereditary disease			
KW Araf-1			
KW XL			
KW K160R			
OS Homo sapiens.			
PN W0200100827-A1.			
XX PN W0200100827-A1.			
XX PD 04-JAN-2001.			
XX PP 30-JUN-2000; 2000WO-US018039.			
XX PR 30-JUN-1999; 99US-0141718P.			
XX XX (UNMI) UNIV MICHIGAN.			
XX PI Nunez G, Hu Y;			
XX DR WPI: 2001-112454/12.			
DR N-PSDB; AAA91125.			
PT Compositions for screening apoptosis pathway agonists and antagonists, useful for the treatment and diagnosis of cancer and autoimmune diseases, Disclosure; Fig 35; 101pp; English.			
PT comprises new splice variants of wild-type Apaf-1 gene.			
XX Sequence 1248 AA;			
CC This sequence represents an Apaf-1 variant of the invention. The variants of the invention are all splice variants of a wild-type Apaf-1 gene (a mammalian homolog of CED-4 that participates in cytochrome c-dependent activation of caspase-3). The DNA is useful in screening assays for identifying apoptosis signalling pathway (ant)agonist, which are in turn useful as potential therapeutics and diagnostic or prognostic tools for diverse types of cancers, autoimmune diseases and hereditary diseases and other members of the signalling pathway, i.e. their substrates or ligands. The protein encoded by the Apaf-1 variant genes are useful in a cell-free assay system and the antibody generated to the translation product are used in immunoprecipitation to isolate new Apaf-1 pathway constituents or their natural mutants			
CC Sequence 1248 AA;			
Query Match 100.0%; Score 6616; DB 4;			
Best Local Similarity 99.9%; Pred. No. 0;			
Matches 1247; Conservative 1; Mismatches 0;			
Indels 0; Gaps 0;			
1 MDAAARNCLCILORREALKDITKTSYMDHNTISDGFLTISEEKVNPTECOORAAMIKM 1			

Db	1 MDAKARNLLQHREALEFDIKTSYIMDHISDGFLTSEEVKRNEPTQQORAAMLIKMI 60	Db	1081 FVCHQGTVLSCDISHDATKFSSTSADDTAKIWSFFDILLPLPHELRGHNGCYRCSAFSVDST 1140
Qy	61 LKKNDNSYSPYNALLHEGYKDAAALHDGIPVSSSSGKDSVSGITSYRTVLCEGGVP 120	Qy	1141 LLATGDNGBTRIWNVSNGELLHLCAPLSBGAATHGGWWTDLCSPDGMNLISAGGYIK 1200
Db	61 LKKNDNSYSPYNALLHEGYKDAAALHDGIPVSSSSGKDSVSGITSYRTVLCEGGVP 120	Db	1141 LLATGDNGBTRIWNVSNGELLHLCAPLSBGAATHGGWWTDLCSPDGMNLISAGGYIK 1200
Qy	121 QRPVVPTVRKLVLNAIQQKLSQLKKGPSWTHGMAGCKSVLAABAFRDHSILEGGCPG 180	Qy	1201 WNNVTGESSIONFTYNTGNLKKIHSPDFKTYVTVNLGLTLYIOLQTLIS 1248
Db	121 QRPVVPTVRKLVLNAIQQKLSQLKKGPSWTHGMAGCKSVLAABAFRDHSILEGGCPG 180	Db	1201 WNNVTGESSIONFTYNTGNLKKIHSPDFKTYVTVNLGLTLYIOLQTLIS 1248
Db	181 GYHWSYKGQDKSGLMLQNLCTRQDEFSQRPLNTEBAKDLRLMLRKPRSLI 240	RESULT 5	AAY97639 standard; protein; 1248 AA.
Db	181 GVHWVSYKGQDKSGLMLQNLCTRQDEFSQRPLNTEBAKDLRLMLRKPRSLI 240	ID	AAY97639 standard; protein; 1248 AA.
Qy	241 ILLDDWDWSWIKAFDSQCQLITTRDKSVDTSVMGPKXWVESSIGKEKGLEIISLFVN 300	XX	XX
Db	241 ILLDDWDWSWIKAFDSQCQLITTRDKSVDTSVMGPKXWVESSIGKEKGLEIISLFVN 300	DT	20-APR-2001 (first entry)
Qy	301 MKKADLPEQAHSLIKECKGSPLVSVLJGALLRDFPNRWEYKLQQLQNKQFKRKSSYD 360	XX	Apaf-1XL-M368L protein sequence.
Db	301 MKKADLPEQAHSLIKECKGSPLVSVLJGALLRDFPNRWEYKLQQLQNKQFKRKSSYD 360	DE	Apaf-1; CED-4 homologue; cytochrome c-dependent activation; caspase-3;
Qy	361 YEALDBAMSISVEMREDIDQYDVTDSLQDKVPTKVLCILWMETEEVDIQLQFN 420	KW	apoptosis signalling pathway; cancer; autoimmune disease; variant; hereditary disease; Apaf-1XL-M368L.
Db	361 YEALDBAMSISVEMREDIDQYDVTDSLQDKVPTKVLCILWMETEEVDIQLQFN 420	KW	Homo sapiens.
Qy	421 KSSLFCDRNGGSFRYTLHDLOVDFLTBKNCSQLDHLKIKLTOFORYHOPHTLSDQEDC 480	OS	XX
Db	421 KSSLFCDRNGGSFRYTLHDLOVDFLTBKNCSQLDHLKIKLTOFORYHOPHTLSDQEDC 480	PN	WO200100827-A1.
Qy	481 MYWWNPFLAYHMASAKNHKELCALMFSLDWIKAKTELVLGAHLIHFVEYRHILDEKDCAV 540	XX	XX
Db	481 MYWWNPFLAYHMASAKNHKELCALMFSLDWIKAKTELVLGAHLIHFVEYRHILDEKDCAV 540	PD	04-JAN-2001.
Qy	541 SENQFQFLSLNGLLGRQPPNIVQGLCEPSETSEVYQOAKLQAOEVNGMLYLEWINK 600	XX	XX
Db	541 SENQFQFLSLNGLLGRQPPNIVQGLCEPSETSEVYQOAKLQAOEVNGMLYLEWINK 600	PP	30-JUN-2000; 2000WO-US018039.
Qy	601 KNITNLSSRLVVRPHTDAVYHACFSEQRASCGADKTLOVKAFTEGKLEIKAHEDEV 660	XX	XX
Db	601 KNITNLSSRLVVRPHTDAVYHACFSEQRASCGADKTLOVKAFTEGKLEIKAHEDEV 660	PR	30-JUN-1999; 99US-0141718P.
Qy	661 LCCAFSTDRETFATCSYDKKVKIWNSTMGTGELVHTDEHSEQVNCCHTFTNSHHILLATGS 720	PA	(UNMI) UNIV MICHIGAN.
Db	661 LCCAFSTDRETFATCSYDKKVKIWNSTMGTGELVHTDEHSEQVNCCHTFTNSHHILLATGS 720	PI	Nunez G, Hu Y;
Qy	721 SDCPLKLWDLNQKECRNTMFHTNSYHCRSPDDKLASASADGTKLWDATSNERKS 780	XX	XX
Db	721 SDCPLKLWDLNQKECRNTMFHTNSYHCRSPDDKLASASADGTKLWDATSNERKS 780	PS	WPI; 2001-112454/12.
Qy	781 INVKQFLNLEDQPEIMEVTKCCSWISADGARIMYAAKNIKFLFDIHTSGLGEHTGH 840	XX	DR
Db	781 INVKQFLNLEDQPEIMEVTKCCSWISADGARIMYAAKNIKFLFDIHTSGLGEHTGH 840	XX	N-PSDB; AAA91118.
Qy	841 STIQYCDFSPOHFLAVALSOYCVELWNTDSRSKVAADCGRHLSWYHGMSPDGSSEFLTS 900	CC	Compositions for screening apoptosis pathway agonists and antagonists, compositions for treatment and diagnosis of cancer and autoimmune diseases, and
Db	841 STIQYCDFSPOHFLAVALSOYCVELWNTDSRSKVAADCGRHLSWYHGMSPDGSSEFLTS 900	CC	mammalian homolog of CBD-4 that participates in cytochrome c-dependent activation of caspase-3. The DNA is useful in screening assays for identifying apoptosis signalling pathway (ant)agonists which are in turn useful as potential therapeutics and diagnostic or prognostic tools for diverse types of cancers, autoimmune diseases and hereditary diseases and
Qy	901 SDDQTIRLWETPKVKCNSAVALKQETDVFOENEWMLAHDHIRLQLINGRTGOLDLT 960	CC	for screening compounds that modulates the interaction of Apaf-1 with other members of the signalling pathway, i.e. their substrates or ligands. The protein encoded by the Apaf-1 variant genes are useful in a cell-free assay system and the antibody generated by the translation product are used in immunoprecipitation assays to isolate new Apaf-1
Db	901 SDDQTIRLWETPKVKCNSAVALKQETDVFOENEWMLAHDHIRLQLINGRTGOLDLT 960	CC	pathway constituents or their natural mutants.
Qy	961 EAQVSCCLCSPLHQLTAFGDNGATEIILLYNNRFQSRFHOKKTVWHIOFTADEKTLIS 1020	SQ	Sequence 1248 AA;
Db	961 EAQVSCCLCSPLHQLTAFGDNGATEIILLYNNRFQSRFHOKKTVWHIOFTADEKTLIS 1020	Query Match	100.0%; Score 6616; DB 4; Length 1248;
Qy	1021 SDDARBIQYNNWQLDKCIERGHQESTKIDPLKNSRLSMSPDGTVKWNITIGNCED 1080	Best Local Similarity	99.9%; Pred. No. 0;
Db	1021 SDDARBIQYNNWQLDKCIERGHQESTKIDPLKNSRLSMSPDGTVKWNITIGNCED 1080	% Matches	1; Mismatches 0; Indels 0; Gaps 0;
Qy	1081 FVCHQGTVLSCDISHPATKESSTSADDTAKIWSFDILLPLPHELRGHNGCYRCASFVSDST 1140	Qy	1 MDAKARNCLQHREALEKDITSYMDHMISDGFTLTSIEBEKVRNEPTQQRAAMLIKMI 60
Db	1081 FVCHQGTVLSCDISHPATKESSTSADDTAKIWSFDILLPLPHELRGHNGCYRCASFVSDST 1140	Db	1 MDAKARNCLQHREALEKDITSYMDHMISDGFTLTSIEBEKVRNEPTQQRAAMLIKMI 60
Qy	61 LKKNDNSYSPYNALLHEGYKDAAALHDGIPVSSSSGKDSVGTSYRTVLCEGGVP 120	Qy	61 LKKNDNSYSPYNALLHEGYKDAAALHDGIPVSSSSGKDSVGTSYRTVLCEGGVP 120

Db	61	LLATGDDNGEIRIWNVSNGELLHLHCAPISEGAATHGCGWVTDLCFS PDGRMLISAGGYIK 1200	Db	1141	LLATGDDNGEIRIWNVSNGELLHLHCAPISEGAATHGCGWVTDLCFS PDGRMLISAGGYIK 1200
Qy	1221	QRPVVFTRKLYNAIQQLSKLKGEPRTVTDHSSLEGCPG 180	Qy	1201	WWNVTGESSQIFYTNGTNLKHKHVS PDKTKYTVVDNLIGLYLQITLE 1248
Db	1221	QRPVVFTRKLYNAIQQLSKLKGEPRTVTDHSSLEGCPG 180	Db	1201	WWNVTGESSQIFYTNGTNLKHKHVS PDKTKYTVVDNLIGLYLQITLE 1248
Qy	1831	GHHVSVSKEQDKSGLUMKLONLCLRDODESFQRPLNTEAKDRRLMRLKHPSSLL 240	Qy	1201	WWNVTGESSQIFYTNGTNLKHKHVS PDKTKYTVVDNLIGLYLQITLE 1248
Db	1831	GHHVSVSKEQDKSGLUMKLONLCLRDODESFQRPLNTEAKDRRLMRLKHPSSLL 240	Db	1201	WWNVTGESSQIFYTNGTNLKHKHVS PDKTKYTVVDNLIGLYLQITLE 1248
Qy	241	ILDDWWSWVKAQFDQCCILLTRDKSVTDSVMPGKXVVEVSSLGKKGLEILSLFVN 300	Qy	1201	WWNVTGESSQIFYTNGTNLKHKHVS PDKTKYTVVDNLIGLYLQITLE 1248
Db	241	ILDDWWSWVKAQFDQCCILLTRDKSVTDSVMPGKXVVEVSSLGKKGLEILSLFVN 300	Db	20-APR-2001	(first entry)
Qy	3031	MKCADLPFQAISIIEKECKGSPLVLSIGALIDFPRKWEYLKQQLQNKOFKRKSSYD 360	Qy	XX	Apaf-1XL-B39Q protein sequence.
Db	3031	MKCADLPFQAISIIEKECKGSPLVLSIGALIDFPRKWEYLKQQLQNKOFKRKSSYD 360	Db	XX	Apaf-1 homologue; cytochrome c-dependent activation; caspase-3;
Qy	3631	YEALDEA <u>S</u> YEMEREDIDYTDLSLQKDVKVPTKVLCILNDMEETEVEDILQEFVN 420	Qy	XX	apoptosis signalling pathway; cancer; autoimmune disease; variant; hereditary disease; Apaf-1XL-B39Q.
Db	3631	YEALDEA <u>S</u> YEMEREDIDYTDLSLQKDVKVPTKVLCILNDMEETEVEDILQEFVN 420	Db	XX	Homo sapiens.
Qy	4231	KSLIFCDRNGKSFRYTLHDLOQDFLTENCSQOLDLHKKITQFORTYQPHLSPDQDC 480	Qy	XX	OS
Db	4231	KSLIFCDRNGKSFRYTLHDLOQDFLTENCSQOLDLHKKITQFORTYQPHLSPDQDC 480	Db	XX	XX
Qy	4831	MYNNFLAYHNASAKOHKECALMFSLWIKAKTELVGPAHLIPEVYRHLIDEDCAV 540	Qy	XX	PN
Db	4831	MYNNFLAYHNASAKOHKECALMFSLWIKAKTELVGPAHLIPEVYRHLIDEDCAV 540	Db	04-JAN-2001.	PD
Qy	5431	SENFOETLSLNGHLLGROPPNTIVQLGICPEPETSEVYQQAKLQAKQEVVDNGMLYLEWINK 600	Qy	XX	XX
Db	5431	SENFOETLSLNGHLLGROPPNTIVQLGICPEPETSEVYQQAKLQAKQEVVDNGMLYLEWINK 600	Db	30-JUN-2000;	2000WO-US018039.
Qy	6031	KNTTNRLLRVPRHTDAVTAHACEDGORIAQSGADKTLQYKATGEKLLKIAKEDEV 660	Qy	XX	XX
Db	6031	KNTTNRLLRVPRHTDAVTAHACEDGORIAQSGADKTLQYKATGEKLLKIAKEDEV 660	Db	XX	XX
Qy	6631	LCCAFSTDPRFLATSVDKVKVWNMSMTGELVHTDEHSEQVNCHFTNSHLLIATGS 720	Qy	XX	PR
Db	6631	LCCAFSTDPRFLATSVDKVKVWNMSMTGELVHTDEHSEQVNCHFTNSHLLIATGS 720	Db	XX	XX
Qy	7231	SDPFLKLWDLNQKECRNTMFGHTNSVNHCRSPDDKLASCADGTLKLWDTSANERKS 780	Qy	XX	XX
Db	7231	SDPFLKLWDLNQKECRNTMFGHTNSVNHCRSPDDKLASCADGTLKLWDTSANERKS 780	Db	XX	This sequence represents an Apaf-1 variant of the invention. The variants of the invention are all splice variants of a wild-type Apaf-1 gene (a mammalian homolog of CED-4) that participates in cytochrome c-dependent activation of caspase-3). The DNA is useful in screening assays for identifying apoptosis signalling pathway (ant)agonists, which are in turn useful as potential therapeutics and diagnostic or prognostic tools for diverse types of cancers, autoimmune diseases and hereditary diseases and for screening compounds that modulates the interaction of Apaf-1 with other members of the signalling pathway, i.e. their substrates or ligands. The protein encoded by the Apaf-1 variant genes are useful in a cell-free assay system and the antibody generated to the translation pathway constituents or their natural mutants
Qy	7831	INYKQFFPLNLDPQDEMTEVVKCCSWADGARIMYAAKWKFLDIHTSGLGEIHTGH 840	Qy	XX	Sequence 1248 AA;
Db	7831	INYKQFFPLNLDPQDEMTEVVKCCSWADGARIMYAAKWKFLDIHTSGLGEIHTGH 840	Db	XX	Disclosure: Fig 32; 101PP; English.
Qy	8431	STIQQCDFSPOHNLAVALSQCVCVELNTDSRSKVDADCRHLSWVHGMSFSDGSSFLTS 900	Qy	XX	WPI: 2001-112454/12.
Db	8431	STIQQCDFSPOHNLAVALSQCVCVELNTDSRSKVDADCRHLSWVHGMSFSDGSSFLTS 900	Db	XX	N-PSDB; AAA91122.
Qy	9031	SDQQTBLWETKVKCNSAVMLQEQDVFQENEOMLAHDRLQLINGTGQDYL 960	Qy	XX	DR
Db	9031	SDQQTBLWETKVKCNSAVMLQEQDVFQENEOMLAHDRLQLINGTGQDYL 960	Db	XX	XX
Qy	9631	EAQVSCCLSPHOTYTAPEDENGAIEILEYVNRIFQSFRQHKTVWHIQFTADEKTLIS 1020	Qy	XX	XX
Db	9631	EAQVSCCLSPHOTYTAPEDENGAIEILEYVNRIFQSFRQHKTVWHIQFTADEKTLIS 1020	Db	XX	XX
Qy	10231	SSDAAEIQWNWQLDKCITPLRGHQETYKDFFLQNSRLISWSPDGTVKWNITGENKEKD 1080	Qy	1	MDAKARNCLQHREALEKDITSYIMDHMISDGFLLISBEBKVNNEPTQOQRAJLJKMI 60
Db	10231	SSDAAEIQWNWQLDKCITPLRGHQETYKDFFLQNSRLISWSPDGTVKWNITGENKEKD 1080	Db	1	MDAKARNCLQHREALEKDITSYIMDHMISDGFLLISBEBKVNNEPTQOQRAJLJKMI 60
Qy	10831	FVCHQGTVLSDCISHDATKPSSTSADKTAKWSPDILLPHLHERGNGCVTCASAFVDT 1140	Qy	61	LKKDNDSYSYSTYNALLHEGKODIAALHGDIPVYVTSYVRTVLCBGGVP 120
Db	10831	FVCHQGTVLSDCISHDATKPSSTSADKTAKWSPDILLPHLHERGNGCVTCASAFVDT 1140	Db	61	LKKDNDSYSYSTYNALLHEGKODIAALHGDIPVYVTSYVRTVLCBGGVP 120
Qy	11431	LLATGDDNGEIRIWNVSNGELLHLHCAPISEGAATHGCGWVTDLCFS PDGRMLISAGGYIK 1200	Qy	121	QRPVVFTRKLVNAIQQKLSKUKGPFWVTHGMAGCGKSVLAEEVRDHSLEGCFFP 180

121	QRPVVFTRKKLYNAIQQLSLKKGEPWVHTGMAGGCKSVLAEARDSLLEGPPG	180	Db	1201	WWVVVTGESSQPFYTYTGTNLKKIHKVSPDFKTYTVTDNLGILYLTQLE	1248
/						
181	GHHWVGQDKSCLLMQLNQLCTRLDODESFSQLPLNTEAKDRRLRILMURKHPRSSL	240		RESULT 7		
	GVRVSVQDKSCLLMQLNQLCTRLDODESFSQLPLNTEAKDRRLRILMURKHPRSSL	240		AAY97644		
181	GVRVSVQDKSCLLMQLNQLCTRLDODESFSQLPLNTEAKDRRLRILMURKHPRSSL	240		ID AAY97644 standard; protein; 1248 AA.		
				XX		
241	ILDDWDWSVLKAFDSCQQLLTRDKSVDTSWMPKVVPVESSLGKEKGFLFILSLPVN	300		AC AAY97644;		
				XX		
241	ILDDWDWSVLKAFDSCQQLLTRDKSVDTSWMPKVVPVESSLGKEKGFLFILSLPVN	300		XX DT 20-APR-2001 (First entry)		
				XX		
301	MKRADLPQSAHSIIKECGSPSPLVSLGALLRDPFNKEVYKLQLQNQFRKIRKSSYD	360		XX DE Apaf-1XL-K63Q protein sequence.		
				XX		
301	KSLIFCDNGKSFRYLHDLQDFLTLTKNSQSLDHLKKITOFQYHQPHTLSPDODC	480		XX KW Apaf-1; CED-4 homologue; cytochrome c-dependent activation; caspase-3;		
				XX KW apoptosis signalling pathway; cancer; autoimmune disease; variant;		
361	YEALDEAMNSIVSEMRLREDIKDYTTDSLQLQDKYKVPTKVLCLIMDMETEVEDILQEFVN	420		XX hereditary disease; Apaf-1XL-K63Q.		
				XX		
361	YEALDEAMNSIVSEMRLREDIKDYTTDSLQLQDKYKVPTKVLCLIMDMETEVEDILQEFVN	420		OS Homo sapiens.		
				XX		
421	KSLIFCDNGKSFRYLHDLQDFLTLTKNSQSLDHLKKITOFQYHQPHTLSPDODC	480		XX PN WO200100827-A1.		
				XX		
421	KSLIFCDNGKSFRYLHDLQDFLTLTKNSQSLDHLKKITOFQYHQPHTLSPDODC	480		XX PD 04-JAN-2001.		
				XX		
481	MWTWNFLAHMASAKMHCALMPSLWIKAKTELVCPAHLTHEFVYRHLDEKCAV	540		XX PR 30-JUN-2000; 2000WO-US018039.		
				XX		
481	MWTWNFLAHMASAKMHCALMPSLWIKAKTELVCPAHLTHEFVYRHLDEKCAV	540		XX PR 30-JUN-1999; 99US-0141718P.		
				XX		
541	SENQFEETSLANGHILLGRQFPNTPVQLGICEPETSEVYQAOALKQAEQFDNGMLELENK	600		XX PA (UNMI) UNIV MICHIGAN.		
				XX		
541	SENQFEETSLANGHILLGRQFPNTPVQLGICEPETSEVYQAOALKQAEQFDNGMLELENK	600		XX Xunz G, Hu Y;		
				XX		
601	KNTNLSSLVVRPHTDAYTAHFCSEDGQRIASGADCKLQVEKAETGSKLLKIAHDEV	660		XX XPI 2001-112454/12.		
				XX DR N-PSDB; AAA91123.		
601	KNTNLSSLVVRPHTDAYTAHFCSEDGQRIASGADCKLQVEKAETGSKLLKIAHDEV	660		XX		
				XX PT Compositions for screening apoptosis pathway agonists and antagonists,		
661	LCCAFSTDRFIATCSVKVTKVWNSTMGLVITYDEVSBEQNCCHTNSHLLATGS	720		XX PT useful for the treatment and diagnosis of cancer and autoimmune diseases,		
				XX PT comprises new splice variants of wild-type Apaf-1 gene.		
661	LCCAFSTDRFIATCSVKVTKVWNSTMGLVITYDEVSBEQNCCHTNSHLLATGS	720		XX Disclosure; Fig 33; 101pp; English.		
				XX		
721	SDCFLKWDLNQKECRTMFEGHTNSVHICRFSPDDKLLASCADGTLKWDATSANERKS	780		XX This sequence represents an Apaf-1 variant of the invention. The variants		
				CC of the invention are all splice variants of a wild-type Apaf-1 gene (a		
721	SDCFLKWDLNQKECRTMFEGHTNSVHICRFSPDDKLASCADGTLKWDATSANERKS	780		CC mammalian homolog of CED-4 that participates in cytochrome c-dependent		
				CC activation of caspase-3). The DNA is useful in screening assays for		
781	TINYQQFFNLDQEDMIVTIVKCCSWMSADGARTMAANKNIFLDIHTSGLGEIHTGHH	840		CC identifying apoptosis signalling pathway (ant)agonists, which are in turn		
				CC useful as potential therapeutics or prognostic tools for		
781	TINYQQFFNLDQEDMIVTIVKCCSWMSADGARTMAANKNIFLDIHTSGLGEIHTGHH	840		CC diverse types of cancers, autoimmune diseases and hereditary diseases and		
				CC for screening compounds that modulates the interaction of Apaf-1 with		
841	STIQYCDSDPQNLLAVVLSQTCVELNTDSSKVAORGHLISWHVGMFSPDGSSLTS	900		CC other members of the signalling pathway, i.e. their substrates or		
				CC ligands. The protein encoded by the Apaf-1 variant genes are useful in a		
841	STIQYCDSDPQNLLAVVLSQTCVELNTDSSKVAORGHLISWHVGMFSPDGSSLTS	900		CC cell-free assay system and the antibody generated to the translation		
				CC product are used in immunoprecipitation assays to isolate new Apaf-1		
901	SDPQTIRLWETKKVCKVNSAVMJKQEVYDVVFQENEVMYLAVDEIRRLQLINGRTQIDLT	960		CC pathway constituents or their natural mutants		
				XX		
901	SDPQTIRLWETKKVCKVNSAVMJKQEVYDVVFQENEVMYLAVDEIRRLQLINGRTQIDLT	960		Sequence 1248 AA;		
				SQ		
961	EAQYSCCCLSPHQLQYIARGDENGAIETILEVNRRIFORSPFOHKTKVWHTQFADEKLIS	1020		Query Match 99.9%; Score 6615; DB 4; Length 1248;		
				Best Local Similarity 99.9%; Pred. No. 0;		
961	EAQYSCCCLSPHQLQYIARGDENGAIETILEVNRRIFORSPFOHKTKVWHTQFADEKLIS	1020		Matches 1247; Conservative 1; Mismatches 0; Indels 0; Gaps 0		
1031	SSDAEIQWNVNLDKCFSLHDATKFSSTSADKATKISFDLILPLHELRGINGVRCASFVSDST	1140		61 LKKD1DSYVSPYTNALIHEGYKDAAIHDGIPVYVSSSGKDSVSGITSYRTVLCBEGVP	120	
				1 MDAKARNCLLQREALEKDITKSYMDHMISDGFLITSEEKVRNEPTQQRAMLIKMI	60	
1031	SSDAEIQWNVNLDKCFSLHDATKFSSTSADKATKISFDLILPLHELRGINGVRCASFVSDST	1140		61 LKQD1DSYVSPYTNALIHEGYKDAAIHDGIPVYVSSSGKDSVSGITSYRTVLCBEGVP	120	
				1 MDAKARNCLLQREALEKDITKSYMDHMISDGFLITSEEKVRNEPTQQRAMLIKMI	60	
1031	FVHQGTFLSCDISSHATKFSSTSADKATKISFDLILPLHELRGINGVRCASFVSDST	1140		61 LKKD1DSYVSPYTNALIHEGYKDAAIHDGIPVYVSSSGKDSVSGITSYRTVLCBEGVP	120	
				1 DB		
1031	FVHQGTFLSCDISSHATKFSSTSADKATKISFDLILPLHELRGINGVRCASFVSDST	1140		61 LKQD1DSYVSPYTNALIHEGYKDAAIHDGIPVYVSSSGKDSVSGITSYRTVLCBEGVP	120	
				1 DB		
1141	LLATGDNGEIRIWNVNGELLHICAPLSEEGAAATHGGWYTDLCFSPDGKMLISAGCYIK	1200		121 QRPVVFTRKKLYNAIQQLSLKKGEPWVHTGMAGGCKSVLAEARDSLLEGPPG	180	
				1141 LLATGDNGEIRIWNVNGELLHICAPLSEEGAAATHGGWYTDLCFSPDGKMLISAGCYIK	1200	
1141	LLATGDNGEIRIWNVNGELLHICAPLSEEGAAATHGGWYTDLCFSPDGKMLISAGCYIK	1200		121 QRPVVFTRKKLYNAIQQLSLKKGEPWVHTGMAGGCKSVLAEARDSLLEGPPG	180	
				121 QRPVVFTRKKLYNAIQQLSLKKGEPWVHTGMAGGCKSVLAEARDSLLEGPPG	180	
1201	WWVVVTGESSQPFYTYTGTNLKKIHKVSPDFKTYTVTDNLGILYLTQLE	1248		181 GVHWVGQDKSGSLMMLKLNQICRPLNIEAKDRRLRILMURKHPRSSL	240	

Db 181 GIVHVVSTGRQDGSLIMKQUNLCTRLDDESFQRDPLNEADRLRLLMRHRPSLL 240
 Qy AAY97645 standard; protein; 1248 AA.
 ID AAY97645
 XX
 AC
 XX
 DT 20-APR-2001 (first entry)
 XX
 DE Apaf-1XL-L83A protein sequence.
 XX
 KW Apaf1; CED-4 homologue; cytochrome c-dependent activation; caspase-3;
 KW apoptosis signalling pathway; cancer; autoimmune disease; variant;
 KW hereditary disease; Apaf-1XL-L83A.
 Qy 301 MKAIDLPEQAISIIKECKGSPVLSIGALLDFPRWETYLKQLQONKFIRKSSYD 360
 Db 301 MKAIDLPEQAISIIKECKGSPVLSIGALLDFPRWETYLKQLQONKFIRKSSYD 360
 Qy 361 YEALDEAMSISVEMLREDIKDYTDISILOQDVKUPTKULCILDMETEEVDILQEVN 420
 Db 361 YEALDEAMSISVEMLREDIKDYTDISILOQDVKUPTKULCILDMETEEVDILQEVN 420
 OS Homo sapiens.
 XX
 PN WO200108827-A1.
 Db 421 KSLIFCDRNGKSFRYTLHDLOQDPLTEKNSQDIAHKKTTQFTHQPHLSPDOEDC 480
 Qy 421 KSLIFCDRNGKSFRYTLHDLOQDPLTEKNSQDIAHKKTTQFTHQPHLSPDOEDC 480
 PR 04-JAN-2001.
 XX
 PR 30-JUN-2000; 2000WO-US018039.
 PR 30-JUN-1999; 99US-0141718P.
 XX
 PR (UNMI) UNIV MICHIGAN.
 PA
 PR Nunez G, Hu Y,
 XX
 PR Disclosure: Fig 34; 101PP; English.
 DR WPI: 2001-112454/12.
 DR N-PDB; AA91124.
 XX
 PT Compositions for screening apoptosis pathway agonists and antagonists,
 PT compositions for screening apoptosis pathway antagonists and antagonists,
 PT used for the treatment and diagnosis of cancer and autoimmune diseases,
 PT comprises new splice variants of wild-type Apaf-1 gene.
 XX
 PS Disclosure: Fig 34; 101PP; English.

Qy 481 MYWYNFLAYHMASAKOHKECALMFSLDWMIAKRTLVGPAPHLINFEVYRHILBDKDCAV 540
 Db 481 MYWYNFLAYHMASAKOHKECALMFSLDWMIAKRTLVGPAPHLINFEVYRHILBDKDCAV 540
 PR 541 SENFOEPLSLNLHGLGROPPNPNTVOLGICEPTSETYQAKLQAKQEVTDNGLYLEWINK 600
 Qy 541 SENFOEPLSLNLHGLGROPPNPNTVOLGICEPTSETYQAKLQAKQEVTDNGLYLEWINK 600
 DB 541 SENFOEPLSLNLHGLGROPPNPNTVOLGICEPTSETYQAKLQAKQEVTDNGLYLEWINK 600
 PR 601 KNITNLSRVYVRPHTDAYHACFSESDGORIASCGADKTLQVKAFETGEKKLIEKAHDEV 660
 Db 601 KNITNLSRVYVRPHTDAYHACFSESDGORIASCGADKTLQVKAFETGEKKLIEKAHDEV 660
 PR 661 LCCAFSTDDRFLATCSVDKVKWNMSITGELVHTYDEHSEQNCHFTNSSHLLATGS 720
 Db 661 LCCAFSTDDRFLATCSVDKVKWNMSITGELVHTYDEHSEQNCHFTNSSHLLATGS 720
 Qy 721 SDPFLKLWDLNQKECRNTMFGHNSVNCRTPSPDDLLASCASGTLKLWDTSAEKRS 780
 Db 721 SDPFLKLWDLNQKECRNTMFGHNSVNCRTPSPDDLLASCASGTLKLWDTSAEKRS 780
 PR 781 INVKQFFFLNITLSDPQDMEVTKGCCSWSDAGARIMVAAKONKFLPDINTHSGLGETHTGH 840
 Db 781 INVKQFFFLNITLSDPQDMEVTKGCCSWSDAGARIMVAAKONKFLPDINTHSGLGETHTGH 840
 PR 841 STIQYCDFSPOHPLAVALSQCYCVELWNTDSRSKYADCRGHLSKVHGMFSPDGSSFLTS 900
 Db 841 STIQYCDFSPOHPLAVALSQCYCVELWNTDSRSKYADCRGHLSKVHGMFSPDGSSFLTS 900
 PR 901 SDQQTFLWPKVKVNSAMMLQEVWDVFNENVLAVDHFERLQJNQGTQDYLTL 960
 Db 901 SDQQTFLWPKVKVNSAMMLQEVWDVFNENVLAVDHFERLQJNQGTQDYLTL 960
 PR 961 EAQVSCCCLSPHLOVIAFEDENGAEILELLNNRIFQSRFHQKCTWVHIOFADEKTLIS 1020
 Db 961 EAQVSCCCLSPHLOVIAFEDENGAEILELLNNRIFQSRFHQKCTWVHIOFADEKTLIS 1020
 PR 1021 SSDDAETOVNWOLDKCIPLRGHQETYKDPLKLNRSRLLSWSFGTQVWNNTGNKEKD 1080
 Db 1021 SSDDAEQQWNWOLDKCIPLRGHQETYKDPLKLNRSRLLSWSFGTQVWNNTGNKEKD 1080
 PR 1081 FVCHOQTVLSCDISDATKFSSTSADTKAKLWSFDLPLPHLRGNGCVRSAFVF DST 1140
 Db 1081 FVCHOQTVLSCDISDATKFSSTSADTKAKLWSFDLPLPHLRGNGCVRSAFVF DST 1140
 PR 1141 LLATGDDNGEERIWVNSGELLHICAPLSECAATHGGNTDLCFSPGKMLISAGYIK 1200
 Db 1141 LLATGDDNGEERIWVNSGELLHICAPLSECAATHGGNTDLCFSPGKMLISAGYIK 1200
 PR 1201 WNVVTCGESOFTYINGTNLKLHVSPDFKCYTVTDNLGLYLTQTL 1248
 Db 1201 WNVVTCGESOFTYINGTNLKLHVSPDFKCYTVTDNLGLYLTQTL 1248
 PR 181 GHFWVSYGVGKODKGSKLGMKLNQNLCTRLDQDESFSQRPLNITEAKDRLLIMARKHRSLL 240
 Db 181 GHFWVSYGVGKODKGSKLGMKLNQNLCTRLDQDESFSQRPLNITEAKDRLLIMARKHRSLL 240
 PR 241 ILDDVNDSWLWKAQFSQCOQILITTRDKSVTDSVMGPKVYYVPESSLGKEKGLEILSLFVN 300

Db	241	ILDDWDSDWVLUKAQFDSQCQIJLITRKSTVSVMGPKVYVVYESSTGKKGLEIISLFVN	300	XX	20-APR-2001 (first entry)
Qy	301	MKKADLPF QASIIIKEKGSPLVLSLGALIIRDPFTRWEYLKQKLNQKFKRKISSYD	360	DT	ApaF-1XL-110A protein sequence.
Db	301	MKKADLPF QASIIIKEKGSPLVLSLGALIIRDPFTRWEYLKQKLNQKFKRKISSYD	360	XX	
Qy	301	MKKADLPF QASIIIKEKGSPLVLSLGALIIRDPFTRWEYLKQKLNQKFKRKISSYD	360	KW	ApaF1; CED-4 homologue; cytochrome c-dependent activation; caspase-3; apoptosis signalling pathway; cancer; autoimmune disease; variant; hereditary disease; Apaf-1XL-110A.
Db	361	YEALDEAMSIISYEMRLREDKQYXTDLSILOKDVKYPTKVICLWDMETEYEDLQEFLVN	420	KW	
Db	361	YEALDEAMSIISYEMRLREDKQYXTDLSILOKDVKYPTKVICLWDMETEYEDLQEFLVN	420	KW	
Db	361	YEALDEAMSIISYEMRLREDKQYXTDLSILOKDVKYPTKVICLWDMETEYEDLQEFLVN	420	XX	
Db	421	KSLIFCDRNGKSPRYYLHDLQVDLPETEKNCNSQOLDLKIKLITOFORYHQPHTLSPQEDC	480	OS	Homo sapiens.
Qy	421	KSLIFCDRNGKSPRYYLHDLQVDLPETEKNCNSQOLDLKIKLITOFORYHQPHTLSPQEDC	480	XX	
Db	421	KSLIFCDRNGKSPRYYLHDLQVDLPETEKNCNSQOLDLKIKLITOFORYHQPHTLSPQEDC	480	PN	WO200100827-A1.
Qy	481	MYWYNFLAYHMASAKHKELCALMFSLWIKARTELVPGPAHLIETVEYHILDEKDCAV	540	XX	
Db	481	MYWYNFLAYHMASAKHKELCALMFSLWIKARTELVPGPAHLIETVEYHILDEKDCAV	540	PD	04-JAN-2001.
Qy	541	SENOFPLSLNGLJGRGPFPNTIVOLGLCEPETSEYVQOAKLQAOEVNGMLYLEWINK	600	XX	
Db	541	SENOFPLSLNGLJGRGPFPNTIVOLGLCEPETSEYVQOAKLQAOEVNGMLYLEWINK	600	XX	
Qy	601	KNITNLRSRIVVRPHTDAVYHACPSEDGQRRIASCADKTLYQPKAETGEKLEIAKEDEV	660	PI	Nunez G, Hu Y;
Db	601	KNITNLRSRIVVRPHTDAVYHACPSEDGQRRIASCADKTLYQPKAETGEKLEIAKEDEV	660	XX	
Qy	661	LCCAFSTD DRPFATCSVDKRYKIWSNMGTGVHTYDHSBEGVNCCHFTNSHLLATGS	720	XX	WPI; 2001-112454/12.
Db	661	LCCAFSTD DRPFATCSVDKRYKIWSNMGTGVHTYDHSBEGVNCCHFTNSHLLATGS	720	XX	N-PSDB; AAA91120.
Qy	721	SDCFKLWLDNQKECRNTMFHTNSYTHCRSPDDKLASCADGTLKLWDATSANERKS	780	XX	
Db	721	SDCFKLWLDNQKECRNTMFHTNSYTHCRSPDDKLASCADGTLKLWDATSANERKS	780	CC	This sequence represents an Apaf-1 variant of the invention. The variants of the invention are all splice variants of a wild-type Apaf-1 gene (a mammalian homolog of CED-4 that participates in cytochrome c-dependent activation of caspase-3). The DNA is useful in screening assays for identifying apoptosis signalling pathway (ant) agonists, which are in turn useful as potential therapeutics or prognostic tools for diverse types of cancers, autoimmune diseases and hereditary diseases and for screening compounds that modulates the interaction of Apaf-1 with other members of the signalling pathway, i.e. their substrates or ligands. The protein encoded by the Apaf-1 variant genes are useful in a cell-free assay system and the antibody generation assays to isolate new Apaf-1 product are used in immunoprecipitation assays to isolate new Apaf-1 pathway constituents or their natural mutants.
Db	781	INVKQPFNLNDPQEDMEVTKCCSWSADGARIMVAAKNKFLDPIHTSGLGEIHTGH	840	CC	
Qy	781	INVKQPFNLNDPQEDMEVTKCCSWSADGARIMVAAKNKFLDPIHTSGLGEIHTGH	840	CC	
Db	781	INVKQPFNLNDPQEDMEVTKCCSWSADGARIMVAAKNKFLDPIHTSGLGEIHTGH	840	CC	
Qy	841	STIQYQCDSPONHLAVALSQYCVELWNTDSRSKVADCRGHLSWHGMSPDGSEFLTS	900	CC	
Db	841	STIQYQCDSPONHLAVALSQYCVELWNTDSRSKVADCRGHLSWHGMSPDGSEFLTS	900	CC	
Qy	901	SDDOTIRLWETKVKCKNSAVALKQEQYDVFOENEMVLAVIDHIRQLQINGRTGQIDYL	960	CC	
Db	901	SDDOTIRLWETKVKCKNSAVALKQEQYDVFOENEMVLAVIDHIRQLQINGRTGQIDYL	960	CC	
Qy	961	EAQVSCCCLSPHLOTAFGDENGATEILELYVNRIFQSFQHKCTVWHIQTADDEKTLIS	1020	CC	
Db	961	EAQVSCCCLSPHLOTAFGDENGATEILELYVNRIFQSFQHKCTVWHIQTADDEKTLIS	1020	CC	
Qy	1021	S3DDAB1QWNWQLDCKCIFLRGHOETVQDFRLLKNSRLLWSFDTGVKWNITCNKEID	1080	Qy	1 MDAKARNCLLQREALEKDITKSYIMDHMTSDGFLTISEEKVNEPTQOORAMILKMI 60
Db	1021	S3DDAB1QWNWQLDCKCIFLRGHOETVQDFRLLKNSRLLWSFDTGVKWNITCNKEID	1080	Db	1 MDAKARNCLLQREALEKDITKSYIMDHMTSDGFLTISEEKVNEPTQOORAMILKMI 60
Qy	1081	FVCHOGTVLSCDISHATKESSTSADKTAIKWSFDLPLHELRGHNCGVRCSAFSV DST	1140	Qy	61 LKKNDTSYTFYNALHHEGYKDLQNLHQDIPVYSSGKDSVSQTSITSYTVTLCSEGVP 120
Db	1081	FVCHOGTVLSCDISHATKESSTSADKTAIKWSFDLPLHELRGHNCGVRCSAFSV DST	1140	Db	61 LKKNDTSYTFYNALHHEGYKDLQNLHQDIPVYSSGKDSVSQTSITSYTVTLCSEGVP 120
Qy	1141	LLATGDDNGEIRIWNVNGELLHICAPLSSEGAAATHGGWTTDLCFSPGKMLISAGGYIK	1200	Qy	121 QRPVVFVTRKLVNIAQQLSKLKEBPGWVTHGAGCKGSVLAEARVDRHSLLGCFPG 180
Db	1141	LLATGDDNGEIRIWNVNGELLHICAPLSSEGAAATHGGWTTDLCFSPGKMLISAGGYIK	1200	Db	121 QRPVVFVTRKLVNIAQQLSKLKEBPGWVTHGAGCKGSVLAEARVDRHSLLGCFPG 180
Qy	1201	WWVVVTGESSQTFYINGTNLKKIRVSPDFKTYVTDNLGLYILOT	1248	Qy	181 GVHWYSGVKDKSGLMKLQNLCTRLDQDESFSQRLPLNITEAKDRLRTILMRKPRSL
Db	1201	WWVVVTGESSQTFYINGTNLKKIRVSPDFKTYVTDNLGLYILOT	1248	Db	181 GVHWYSGVKDKSGLMKLQNLCTRLDQDESFSQRLPLNITEAKDRLRTILMRKPRSL
Qy	241	ILDDWDSDWVLUKAQFDSQCQIJLITRKSTVSVMGPKVYVVYESSTGKKGLEIISLFVN	300	Qy	241 ILDDWDSDWVLUKAQFDSQCQIJLITRKSTVSVMGPKVYVVYESSTGKKGLEIISLFVN
Db	241	ILDDWDSDWVLUKAQFDSQCQIJLITRKSTVSVMGPKVYVVYESSTGKKGLEIISLFVN	300	Db	241 ILDDWDSDWVLUKAQFDSQCQIJLITRKSTVSVMGPKVYVVYESSTGKKGLEIISLFVN
Qy	301	MKKADLPQAHSSITKECKGSPLVYSLIGALLRDFPNRWEYTLKQLQNKQFKRIRSSYD	360	Qy	301 MKKADLPQAHSSITKECKGSPLVYSLIGALLRDFPNRWEYTLKQLQNKQFKRIRSSYD

RESULT 9
 AAY97641 standard; protein: 1248 AA.
 XX AAY97641;
 AC AC

Db	301	MKRADLPSQAHSTIKRGSPLVWSLIGALLRDFPNWEYILQKLNQKPFKRKSSYD	360	XX	Apaf-1 homologue; cytochrome c-dependent activation; caspase-3;
Qy	361	YEALDEAMSISYEMLREDIDYYTDLTLIQLQDVKVPKVLCILIDMTEVEVDILQEVFN	420	KW	apoptosis signalling pathway; cancer; autoimmune disease; variant;-hereditary disease; Apaf-1XL-M368L/K160R.
Db	361	YEALDEAMSISYEMLREDIDYYTDLTLIQLQDVKVPKVLCILIDMTEVEVDILQEVFN	420	KW	autoimmune disease; variant;-hereditary disease; Apaf-1XL-M368L/K160R.
		Homo sapiens.		XX	
Qy	421	KSLIFCDRNGKSPRYTLHDLOQDFITERNCNSQODLHKKLTITOFORYHOPHTLSPDQDC	480	OS	
Db	421	KSLIFCDRNGKSPRYTLHDLOQDFITERNCNSQODLHKKLTITOFORYHOPHTLSPDQDC	480	OS	
Qy	481	MTWYNFLAYHMASAKOHKECALMNSLDWIKAKTELVGPALLINEFVEYRLDKECAV	540	OS	
Db	481	MTWYNFLAYHMASAKOHKECALMNSLDWIKAKTELVGPALLINEFVEYRLDKECAV	540	OS	
Qy	541	SENFQEFISLNLCHLGRQPNNPVLQGCEPETSEYVQAKLQAKQEVDNGMLYEWINK	600	PA	UNM1 UNIV MICHIGAN.
Db	541	SENFQEFISLNLCHLGRQPNNPVLQGCEPETSEYVQAKLQAKQEVDNGMLYEWINK	600	PA	
Qy	601	KNTINLSPLVVRPHTDAAVHACFSBDGORIASGADTLYQFKATGKELLKIAHDEV	660	PA	
Db	601	KNTINLSPLVVRPHTDAAVHACFSBDGORIASGADTLYQFKATGKELLKIAHDEV	660	PA	
Qy	661	LCCAFSTDDRFATCSVDKVKVTKINSMTGELVATYBHSQVNCCFTNSHILLATGS	720	PA	
Db	661	LCCAFSTDDRFATCSVDKVKVTKINSMTGELVATYBHSQVNCCFTNSHILLATGS	720	PA	
Qy	7221	SDCFLKLWDLNOKECRNTMFGHTNSVNCRCFSPDDKILASCASTDGLWDATDSANERKS	780	PA	
Db	7221	SDCFLKLWDLNOKECRNTMFGHTNSVNCRCFSPDDKILASCASTDGLWDATDSANERKS	780	PA	
Qy	7811	INTKQFFFLNLEDPOQEMIVYVKCCSWSDGATIMVAKNCFLDINTSGLGEIHTGHH	840	PA	This sequence represents an Apaf-1 variant of the invention. The variant is of the invention are all splice variants of a wild-type Apaf-1 gene (a mammalian homolog of CED-4 that participates in cytochrome c-dependent activation of caspase-3). The DNA is useful in screening assays for identifying apoptosis signalling pathway (ant) agonists, which are in turn useful as potential therapeutic tools for diverse types of cancers, autoimmune diseases and hereditary diseases and other members of the signalling pathway, i.e. their substrates or ligands. The protein encoded by the Apaf-1 variant genes are useful in a cell-free assay system and the antibody generated to the translation product are used in immunoprecipitation assays to isolate new Apaf-1 pathway constituents or their natural mutants
Db	7811	INTKQFFFLNLEDPOQEMIVYVKCCSWSDGATIMVAKNCFLDINTSGLGEIHTGHH	840	PA	
Qy	841	STIQYCDPSPNHLAVALSQYCVELNTDSKSVKADCRLGHLSVHGTMFSQDGSSFLTS	900	PA	
Db	841	STIQYCDPSPNHLAVALSQYCVELNTDSKSVKADCRLGHLSVHGTMFSQDGSSFLTS	900	PA	
Qy	901	SDQDTIRLWEKVKVCKNSAMMLKOEVDVYFQEENVMVLAHDHIRRLQLINGTQGDYL	960	PA	
Db	901	SDQDTIRLWEKVKVCKNSAMMLKOEVDVYFQEENVMVLAHDHIRRLQLINGTQGDYL	960	PA	
Qy	961	EAQYSCCLSPHLOYTAFGENGIAEILEYVNRRIFQSFRQHKCTVWHIQFADDEKTLIS	1020	PA	
Db	961	EAQYSCCLSPHLOYTAFGENGIAEILEYVNRRIFQSFRQHKCTVWHIQFADDEKTLIS	1020	PA	
Qy	1021	SSDAEIQVWNWOLDKCIFRGHQETYKDFULLKNSRLLSWSEFTGVKVNNTITGNKEKD	1080	PA	
Db	1021	SSDAEIQVWNWOLDKCIFRGHQETYKDFULLKNSRLLSWSEFTGVKVNNTITGNKEKD	1080	PA	
Qy	1081	FVCHQGTVLSCDISDATKESPSADTKATMSFDLPLHELRGHCYRSAPVYST	1140	PA	
Db	1081	FVCHQGTVLSCDISDATKESPSADTKATMSFDLPLHELRGHCYRSAPVYST	1140	PA	
Qy	1141	LITATGDDNGTRIYVNSGELHLICAPLSEGAATHGGMYDLCFSPDGKMLISAGGYIK	1200	PA	
Db	1141	LITATGDDNGTRIYVNSGELHLICAPLSEGAATHGGMYDLCFSPDGKMLISAGGYIK	1200	PA	
Qy	1201	WWVVVTGBESSQTYTGTNLKICHVSPDPKCYVTDNLGLYLQITLE	1248	PA	
Db	1201	WWVVVTGBESSQTYTGTNLKICHVSPDPKCYVTDNLGLYLQITLE	1248	PA	
		RESULT 1.0			
AAV97647		AAV97647 standard; protein: 1248 AA.			
XX					
AC					
XX					
DT	20-APR-2001	(first entry)			
XX					
DE		Apaf-1XL-M368L/K160R protein sequence.			

Page 11

Db 421 KSLIFCDRNGKSFRYLHDQVDTKNCNCSQDHLHKKITQFQRYHQPHFTLSPDQEDC 480
 Qy 482 MYNNFLAYHMASAKMHEKCALMSLDWIKAKTELVPAHLTHFVEYRHTLDEKDCAV 540
 Db 481 MYNNFLAYHMASAKMHEKCALMSLDWIKAKTELVPAHLTHFVEYRHTLDEKDCAV 540
 Qy 541 SENFOEFLSINGHLLGROPPNPNTVOLGICEPETSEYYQQARLQKQETDNGMLYLEWINK 600
 Db 541 SENFOEFLSINGHLLGROPPNPNTVOLGICEPETSEYYQQARLQKQETDNGMLYLEWINK 600
 Qy 601 KNITNLISRLVTRPHDAVHAFCSEDGORIASGADKTLOVKRAFTGEKLLEIKAHEDEV 660
 Db 601 KNITNLISRLVTRPHDAVHAFCSEDGORIASGADKTLOVKRAFTGEKLLEIKAHEDEV 660
 Qy 661 LCCAFSTDDRFATCSVDKCKVTKWNMTGELEYTDEHSFQNVCNCHFTPSHLLATG 720
 Db 661 LCCAFSTDDRFATCSVDKCKVTKWNMTGELEYTDEHSFQNVCNCHFTPSHLLATG 720
 Qy 721 SDQFLKLMWDLNQKECRNTMFGHTNSVHCRFSPPDKLASCSDAQTKLWMDTSANERKS 780
 Db 721 SDQFLKLMWDLNQKECRNTMFGHTNSVHCRFSPPDKLASCSDAQTKLWMDTSANERKS 780
 Qy 781 INYKQFFNLINLDPQEDMEVTKKCCSWSDAGRIMYAAKNCFLDIHTSGLIGEHTIGHH 840
 Db 781 INYKQFFNLINLDPQEDMEVTKKCCSWSDAGRIMYAAKNCFLDIHTSGLIGEHTIGHH 840
 Qy 841 STIQYCDPFSPOHNLAVALSQICVELNTDSKESKADCRGHLSKVHGMFSGDGSPLTS 900
 Db 841 STIQYCDPFSPOHNLAVALSQICVELNTDSKESKADCRGHLSKVHGMFSGDGSPLTS 900
 Qy 901 SDDQTIRLWETTKVCKVCKNSAMVLMKQEVDVVFQENEYMLVAVDTHIRRLQLINGRTQDYL 960
 Db 901 SDDQTIRLWETTKVCKVCKNSAMVLMKQEVDVVFQENEYMLVAVDTHIRRLQLINGRTQDYL 960
 Qy 961 EAQYSCCCLSPHLOTAPEDEENGAEIILEVNRFQSFQHKKTVWHIQFTADEKTLIS 1020
 Db 961 EAQVSCCCLSPHLOTAPEDEENGAEIILEVNRFQSFQHKKTVWHIQFTADEKTLIS 1020
 Qy 1021 SSSDAEIQVNWNWOLDKCIPIRGHQETYDFFRULLKNSRLWSFQGTQVWNNTGNKED 1080
 Db 1021 SSSDAEIQVNWNWOLDKCIPIRGHQETYDFFRULLKNSRLWSFQGTQVWNNTGNKED 1080
 Qy 1081 FVCHQGTVLSCDISDATAKPSPSADKTAKTWSFDLPHLHRGNGCCVROSAPSYDST 1140
 Db 1081 FVCHQGTVLSCDISDATAKPSPSADKTAKTWSFDLPHLHRGNGCCVROSAPSYDST 1140
 Qy 1141 LLATGDDNGTRINNVNSNGELBLFLCAPLSEGAATHGGNYTDLCPSPDGKMLISAGGYIK 1200
 Db 1141 LLATGDDNGTRINNVNSNGELBLFLCAPLSEGAATHGGNYTDLCPSPDGKMLISAGGYIK 1200
 Qy 1201 WNNVVTCGESSTQFTYINGTNLKKHVSPDKEVYTVDNLGLIYLTQLE 1248
 Db 1201 WNNVVTCGESSTQFTYINGTNLKKHVSPDKEVYTVDNLGLIYLTQLE 1248
 Qy 1201 WNNVVTCGESSTQFTYINGTNLKKHVSPDKEVYTVDNLGLIYLTQLE 1248

RESULT 1.2
 AA97638 ID AA97638 standard; protein; 1237 AA.
 XX AAY97638; DT 20-APR-2001 (first entry)
 DE Apaf-1ND protein sequence.

Apaf-1; CED-4 homologue; cytochrome c-dependent activation; caspase-3;
 apoptosis signalling pathway; cancer; autoimmune disease; variant;
 hereditary disease; Apaf-1ND.

XX Homo sapiens.
 XX WO200100827-A1.

Db PD 04-JAN-2001.
 Qy XX 30-JUN-2000; 20000WO-US018039.
 Db PR 30-JUN-1999; 99US-0141718P.
 Qy XX UNIV MICHIGAN.
 Db PA XX
 Qy PI XX
 Db DR XX
 Qy DR N-PSDB; AAS9117.
 Db PT Compositions for screening apoptosis pathway agonists and antagonists useful for the treatment and diagnosis of cancer and autoimmune diseases, comprises new splice variants of wild-type Apaf-1 gene.
 Disclosure: Fig 27: 101pp; English.
 Ps XX
 Qy XX
 This sequence represents an Apaf-1 variant of the invention. The variants of the invention are all splice variants of a wild-type Apaf-1 gene (a mammalian homolog of CED-4 that participates in cytochrome c-dependent activation of caspase-3). The DNA is useful in screening assays for identifying apoptosis signalling pathway (ant) agonists, which are in turn useful as potential therapeutic or prognostic tools for diverse types of cancer, autoimmune diseases and hereditary diseases and for screening compounds that modulates the interaction of Apaf-1 with other members of the signalling pathway, i.e. their substrates or ligands. The protein encoded by the Apaf-1 variant genes are useful in a cell-free assay system and the antibody generated to the translation product used in immunoprecipitation assays to isolate new Apaf-1 pathway constituents or their natural mutants
 Sequence 1237 AA:
 Query Match 98.9%; Score 6548.5; DB 4; Length 1237;
 Best Local Similarity 99.1%; Pred. No. 0; Indels 11; Gaps 1;
 Matches 1237; Conservative 0; Mismatches 0; Indels 11; Gaps 1;
 Qy 1 MDKARNCCLLQHREALEKDITKSYIMDHMISGFLTISEBEKVRNEPTQQQAMLIKMI 60
 Db 1 MDKARNCCLLQHREALEKDITKSYIMDHMISGFLTISEBEKVRNEPTQQQAMLIKMI 60
 Qy 61 LKKDNDSYVSYTNAALLHESYKDLAALHDGFVYFVSSSSGKDSWSGITSYVRTVLCEGVP 120
 Db 61 LKKDNDSYVSYTNAALLHESYKDLAALHDGFVYFVSSSS-----VRTVLCEGVP 109
 Qy 121 QRDNUFTRKJKNMIAQQLSLKLGEGCMWTHMGAGCKSVLAAATRDHSULEGCRPG 180
 Db 110 QREVVFTRKLNATIQQKLKSLQGEPWTHMGAGCKSVLAAATRDHSULEGCRPG 169
 Qy 181 GHFWVSYGKDKSGLMLQNLCTRLODEDFSPLNTEAKDRILMRKHRSLL 240
 Db 170 GHFWVSYGKDKSGLMLQNLCTRLODEDFSPLNTEAKDRILMRKHRSLL 229
 Qy 241 ILDDWDWSWIKLRAFDQSQCLLTTDRKSVTDSVMGPKYVVPVBSLGLKEBLISLFVN 300
 Db 230 ILDDWDWSWIKLRAFDQSQCLLTTDRKSVTDSVMGPKYVVPVBSLGLKEBLISLFVN 289
 Qy 301 MKCADLPQASIIKECKCSPLVSLGALLDPRNRWEYLKQLQNKQFRKRKSSYD 360
 Db 290 MKCADLPQASIIKECKCSPLVSLGALLDPRNRWEYLKQLQNKQFRKRKSSYD 349
 Qy 361 YEALDEAMSISEVMLREDIKDYXTDLSILOKDVKPTKVLCLIMDMETEEVDRDILQEPVN 420
 Db 350 YEALDEAMSISEVMLREDIKDYXTDLSILOKDVKPTKVLCLIMDMETEEVDRDILQEPVN 409
 Qy 421 KSLIFCDRNGKSFRYLLDQVDFLTKNCNCSQDHLHKKITOFQRYHOPLTSPOEDC 480
 Db 410 KSLIFCDRNGKSFRYLLDQVDFLTKNCNCSQDHLHKKITOFQRYHOPLTSPOEDC 469
 Qy 481 MYNNFLAYHMASAKMHEKCALMSLDWIKAKTELVPAHLTHFVEYRHTLDERKCAV 540

Db	470	MYWYNFLAYTHMASAKHKEKCALMPSLSDWIKAKTELVGPALJHEFVBYRHILDEKCAV	529	PD	04-SEP-2003.
Qy	541	SENFQFLSINGHLGRQPFPNTVQLGICPEPSETSEYQQAKIQAOKFVDNGLYLEWINK	600	XX	31-OCT-2002; 2002NO-US035433.
Db	530	SENFQFLSINGHLGRQPFPNTVQLGICPEPSETSEYQQAKIQAOKFVDNGLYLEWINK	589	XX	31-OCT-2001; 2001US-0336220P.
Qy	601	KNITNLSRLYVRPHTDAYHAFCSEQRIASCGADKTLOVKAETGKBLPIKAHDDEV	660	PA	(CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Db	590	KNITNLSRLYVRPHTDAYHAFCSEQRIASCGADKTLOVKAETGKBLPIKAHDDEV	649	XX	Hirsch R, Thornton SL;
Qy	661	LCCAFSTDDEPATCSDKKIKWNSMTGEIWTDEHSEQNCCHTNSHLLATGS	720	XX	DR WPI; 2003-712740/67.
Db	650	LCCAFSTDDEPATCSDKKIKWNSMTGEIWTDEHSEQNCCHTNSHLLATGS	709	XX	DR GENBANK; NP_037361.
Qy	721	SDCFKLKDMLQKRCRNTMFGHTNSYNHCRFSPDKULLASCADGTKLWDATSANERKS	780	PT	Diagnosing and analyzing autoimmune disease using gene expression profiles and microarray technology, useful for diagnosing and treating rheumatoid arthritis, lupus, fibrosis, osteoarthritis, fibromyalgia and gout.
Db	710	SDCFKLKDMLQKRCRNTMFGHTNSYNHCRFSPDKULLASCADGTKLWDATSANERKS	769	PT	PT Disclosure; Page: 56pp; English.
Qy	781	INVKQFPLNLDPQEDMEVITYRCCWSADGARIMVAKNCFLPFDIHTSGLGEITHIGH	840	XX	XX The invention relates to a novel method for diagnosing and analysing a autoimmune disease or arthritides. The method comprises obtaining a patient sample containing mRNA, analysing gene expression using the mRNA that results in a gene expression signature of the mRNA, and using a gene expression signature to diagnose or analyse the autoimmune disease or arthritides in the patient, where gene expression of at least 60% of the genes correlates with that of the gene signature. The invention further comprises: a treatment of rheumatoid arthritis; identification of genes for targeting in the treatment of rheumatoid arthritis in a mammal other than a mouse; diagnosis of rheumatoid arthritis in a mammal, an array or gene chip, specific for rheumatoid arthritis; diagnosis or analyses of autoimmune disease or rheumatoid arthritis; screening the efficacy of a candidate drug in vitro for the treatment of collagen-induced arthritis; and reducing the symptoms associated with collagen-induced arthritis. The compositions of the invention have the following activities: immunosuppressive, antiarthritic, osteopathic, antirheumatic, antigenic, antiinflammatory, dermatological, and immunomodulatory. The methods and compositions of the present invention are useful for diagnosing and treating autoimmune disease or arthritides, such as rheumatoid arthritis, lupus, ankylosing spondylitis, fibrosis, fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an immune disease caused by an infective agent. This sequence represents a protein sequence relating to the genes used in the analysis and treatment of autoimmune diseases or arthritides. Note: This sequence is not shown in the specification. It has been supplied in an electronic format from WIPO.
Db	770	INVKQFPLNLDPQEDMEVITYRCCWSADGARIMVAKNCFLPFDIHTSGLGEITHIGH	829	PS	Sequence 1237 AA;
Qy	841	STIQQDFSPONHLAVALSQCVELANTDERSKVAADCRCGHLSWIVCMFSPDGSSPLTS	900	CC	Query Match 98.9%; Score 6548.5; DB 7; Length 1237;
Db	830	STIQQDFSPONHLAVALSQCVELANTDERSKVAADCRCGHLSWIVCMFSPDGSSPLTS	889	CC	Best Local Similarity 99.1%; Pred. No. 0; Missmatches 0; Indels 11; Gaps 1
Qy	901	SDDQTTRLWTPKVKVCKNSAVMLQEQVDDVVFGENEVAVLAVDHIRRLQLINGRTQDYL	960	CC	Qy 1 MDAKARNCLQHPRALEKDITSYVMDHMISDGFTLTSBEEKVNRNEPTQOQRAAMLIKMI 60
Db	890	SDDQTTRLWTPKVKVCKNSAVMLQEQVDDVVFGENEVAVLAVDHIRRLQLINGRTQDYL	949	CC	Db 1 MDAKARNCLQHPRALEKDITSYVMDHMISDGFTLTSBEEKVNRNEPTQOQRAAMLIKMI 60
Qy	961	EAQVSCCCLSPHQYTAFGDENGATEILEYNNRIFOSRFQHKKTWHIQFTADEKLIS	1020	CC	Qy 2 1 QRPVVFTRKVLQKLNIAIOOKLISKLKEPGPVATIHMGAGCGKSVLAEARVDHSLLGCFFPG 180
Db	1010	SSDDABIQVNWNQLDKCIEFLRQHOTVKDFRLLKNSMALLSFEDGTVKVNNNLTGKKEID	1069	CC	Db 2 110 QRPVVFTRKVLQKLNIAIOOKLISKLKEPGPVATIHMGAGCGKSVLAEARVDHSLLGCFFPG 169
Db	950	EAQVSCCCLSPHQYTAFGDENGATEILEYNNRIFOSRFQHKKTWHIQFTADEKLIS	1009	CC	Qy 3 61 LKCDNDSTSYVSYNALLHEGYKDLAALLHGIPVYSSGKDSVGITSYVRLVLCGGVP 120
Qy	1021	SSDDABIQVNWNQLDKCIEFLRQHOTVKDFRLLKNSMALLSFEDGTVKVNNNLTGKKEID	1080	CC	Db 3 61 LKCDNDSTSYVSYNALLHEGYKDLAALLHGIPVYSSS-----VRVTVLCEGGVP 109
Db	1070	FVCHQGTVLSDCIDHATKFSTSADTKA1KWSFDLPLLPHLRLGRNGCVRCSAFSYDST	1140	CC	Qy 4 181 GHWYSVGQDKSCLIMKLQNLCPRLQDQESFSQPLNITEAKRILRKPRSLI 240
Qy	1141	LLATGDNGEIRIWAYNSNGELIHLHCAPLSEGAATHCGWVTDLCFSFDGKMLISAGGYK	1200	CC	Db 4 170 GHWYSVGQDKSCLIMKLQNLCPRLQDQESFSQPLNITEAKRILRKPRSLI 229
Db	1130	LLATGDNGEIRIWAYNSNGELIHLHCAPLSEGAATHCGWVTDLCFSFDGKMLISAGGYK	1189	CC	Qy 5 241 ILDDWDSSVNLKAEDSOCQILLTRDKSVDTSVNGPKVYPVESSLGKEKGBLBISLFLVN 300
Qy	1201	WWNVYTGEGSSOTEYTINGTNLAKTHYSPDFTKYVTDNLGLYIQLTE	1248	CC	Db 5 230 ILDDWDSSVNLKAEDSOCQILLTRDKSVDTSVNGPKVYPVESSLGKEKGBLBISLFLVN 289
Db	1190	WWNVYTGEGSSOTEYTINGTNLAKTHYSPDFTKYVTDNLGLYIQLTE	1237	XX	OS Homo sapiens.
					PN WO2003072827-A1.
RESULT 13					
ID ADP65308	standard	protein	1237 AA.		
XX					
AC ADP65308;					
XX					
DT 12-AUG-2004	(first entry)				
XX					
DE Human apoptotic protease activating factor isoform A, apoptotic protease.					
XX					
KW autoimmune disease; arthritis; gene expression analysis;					
KW rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic;					
KW antiarthritic; osteopathic; antigenic; antiinflammatory; dermatological;					
KW immunomodulatory; lupus; ankylosing spondylitis; Fibrosis;					
KW fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;					
KW immune; human.					
OS					
XX					
PN					

Qy	301	MKKADLPEQAHSLIKECKGSPLVLSIGALLRDPNPNRVEYYIKQLQNLQKPFIRKSSYD	360	Apoptosis inducer splice variant Apaf-1L.
Db	290	MKKADLPEQAHSLIKECKGSPLVLSIGALLRDPNPNRVEYYIKQLQNLQKPFIRKSSYD	349	Apaf-1L; Apaf-1; splice variant; human; caspase-3; activator; Ced-4; human; apoptosis; programmed cell death; cancer; AIDS; multiple sclerosis; inflammation; therapy.
Qy	361	YEALDEAMSISVEMLREDIKOYITDLSIQLQDKVUPTKVLCLILWDMTEEVBDILOQEFVN	420	
Db	350	YEALDEAMSISVEMLREDIKOYITDLSIQLQDKVUPTKVLCLILWDMTEEVBDILOQEFVN	409	Homo sapiens.
Qy	421	KSLLFCDRNRKSPFVYLLDQLQDFLTKEKNSQDPLHKKITTOFORTHOPTLSPDQEDC	480	OS
Db	410	KSLLFCDRNRKSPFVYLLDQLQDFLTKEKNSQDPLHKKITTOFORTHOPTLSPDQEDC	469	XX
Qy	481	MYWNFLAYMASARMHHLCALMFSLDWIKAKTLYGEPAHLTHEFYBYRHLDEDKCAV	540	Key Peptide
Db	470	NYWNFLAYMASARMHHLCALMFSLDWIKAKTLYGEPAHLTHEFYBYRHLDEDKCAV	529	XX
Qy	541	SENFQOFPSLNGHLLGROPPNIVOLGLCBEETSEVYQAAKLOAQEVNDNLYLEWINK	600	Location/Qualifiers
Db	530	SENFQOFPSLNGHLLGROPPNIVOLGLCBEETSEVYQAAKLOAQEVNDNLYLEWINK	589	99..109 /note= "additional 11 amino acids compared with Apaf-1" 613 ..643 /note= "putative WD repeat" 655 ..685 /note= "putative WD repeat" 692 ..729 /note= "putative WD repeat" 741 ..771 /note= "putative WD repeat" 788 ..825 /note= "putative WD repeat" 928 ..946 /note= "putative WD repeat" 958 ..988 /note= "putative WD repeat" 999 ..1038 /note= "putative WD repeat" 1040 ..1070 /note= "putative WD repeat" 1082 ..1112 /note= "putative WD repeat" 1119 ..1160 /note= "putative WD repeat"
Qy	601	KNTINLSRLVYRPHTDAYTHACPSEDCQRIISCGADKTLQVEAETCEBKLLIKEADEDEV	650	FT Region
Db	590	KNTINLSRLVYRPHTDAYTHACPSEDCQRIISCGADKTLQVEAETCEBKLLIKEADEDEV	649	FT Region
Qy	661	LCCAFSTDDEPIATCSVDOKKVKIWNSTMGTGELVHTYDENESEQNCCHFTNSHHLLIATGS	720	FT Region
Db	650	LCCAFSTDDEPIATCSVDOKKVKIWNSTMGTGELVHTYDENESEQNCCHFTNSHHLLIATGS	709	FT Region
Qy	721	SDCFKLWDLNQKECRNTMFIGHTNSVNHCRSPDDKLASCADGTLKLWDLTSANERKS	780	FT Region
Db	710	SDCFKLWDLNQKECRNTMFIGHTNSVNHCRSPDDKLASCADGTLKLWDLTSANERKS	769	FT Region
Qy	781	INVQPFPLNEDPQDMEVTVCCSNSADGARIMIAAKKTFDPIHTSGLIGEHTGH	840	FT Region
Db	770	INVQPFPLNEDPQDMEVTVCCSNSADGARIMIAAKKTFDPIHTSGLIGEHTGH	829	XX
Qy	841	STIQYCDFSPOHHLAVVLSQCYVELANTDSRSKVADCRGHLSKVHGFMFSPDGSSFLTS	900	W0985615-A1.
Db	830	STIQYCDFSPOHHLAVVLSQCYVELANTDSRSKVADCRGHLSKVHGFMFSPDGSSFLTS	889	XX
Qy	901	SDDQTIRLMETKVKYCNSAVMLKQEVYDVVFQENYMLVAHDHTRLQLINGRTGQDYL	960	PD 10-DEC-1998.
Db	890	SDDQTIRLMETKVKYCNSAVMLKQEVYDVVFQENYMLVAHDHTRLQLINGRTGQDYL	949	XX
Qy	961	EAQVSCCCLSPHQYTAIFGDEGAIELEYLNRFQSREHQKRTVWHIQFADEXTLIS	1020	XX
Db	950	EAQVSCCCLSPHQYTAIFGDEGAIELEYLNRFQSREHQKRTVWHIQFADEXTLIS	1009	PR 05-JUN-1997;
Qy	1021	SSDAETQWWNWLQKCIPLRGEOETYKDTRILLKSRLLWSFGTQVWNITGKEDK	1080	PR 07-AUG-1997;
Db	1010	SSDAETQWWNWLQKCIPLRGEOETYKDTRILLKSRLLWSFGTQVWNITGKEDK	1069	XX
Qy	1081	FVCHQGTVLSCDISDATKFSSSADKTAK1WSFDLPLPHELGRHNGCVRSAFSV DST	1140	PA (GETH) GENENTECH INC . (TEK) UNIV TEXAS .
Db	1070	FVCHQGTVLSCDISDATKFSSSADKTAK1WSFDLPLPHELGRHNGCVRSAFSV DST	1129	XX
Qy	1141	LATGDDNGEIRWVNSGELLHICAPLSEGAATGGWTDLCFSPDGKMLISAGGYK	1200	Zou H, Henzel WJ, Wang X; WPI: 1999-080828/07. DR N-PSDB ; NAV84798.
Db	1130	LATGDDNGEIRWVNSGELLHICAPLSEGAATGGWTDLCFSPDGKMLISAGGYK	1189	XX
Qy	1201	WWVVVTGSESSQFYTGTNKKTHVSPDFTKTVTVDNLGLIYIQLTE	1248	PT New Apaf-1 protein for regulating apoptosis - is a human homologue of Ced-4 and an activator of caspase-3; for screening agents that regulate apoptosis and for treating cancer, AIDS.
Db	1190	WWVVVTGSESSQFYTGTNKKTHVSPDFTKTVTVDNLGLIYIQLTE	1237	PT
Qy	1141	LATGDDNGEIRWVNSGELLHICAPLSEGAATGGWTDLCFSPDGKMLISAGGYK	1200	XX
Db	1130	LATGDDNGEIRWVNSGELLHICAPLSEGAATGGWTDLCFSPDGKMLISAGGYK	1189	CC This polypeptide comprises Apaf-1L, a splice variant of Apaf-1 (see AAW91071). a novel human protein that is believed to be a mammalian homologue of the Caenorhabditis elegans Ced-4 apoptosis protein. Apaf-1L was produced from HeLa cell mRNA. The encoded polypeptide contains 11 additional amino acids compared to Apaf-1, but retains the structural and functional features of Apaf-1. It is a 130 kDa polypeptide containing a Ced-3 homologous N-terminal domain, followed by a Ced-4 homologous domain and multiple C-terminal WD-40 repeats. It forms a complex with cytochrome-3 and activates caspase-3 in the apoptotic pathway. Apaf-1L can be produced by culturing cells transformed or transfected with a vector containing Apaf-1L nucleic acid. Apaf-1L polypeptides, including Apaf-1L, can be used to induce apoptosis, and the polypeptides, genes and antibodies are especially useful for screening and identifying cells signalled for apoptosis. Agonistic antibodies can be used to stimulate apoptosis in cancer cells, and antagonistic antibodies can be used to block excessive apoptosis or to block the
Db	1190	WWVVVTGSESSQFYTGTNKKTHVSPDFTKTVTVDNLGLIYIQLTE	1237	CC
Qy	1141	LATGDDNGEIRWVNSGELLHICAPLSEGAATGGWTDLCFSPDGKMLISAGGYK	1200	CC
Db	1130	LATGDDNGEIRWVNSGELLHICAPLSEGAATGGWTDLCFSPDGKMLISAGGYK	1189	CC
Qy	1201	WWVVVTGSESSQFYTGTNKKTHVSPDFTKTVTVDNLGLIYIQLTE	1248	CC
Db	1190	WWVVVTGSESSQFYTGTNKKTHVSPDFTKTVTVDNLGLIYIQLTE	1237	CC
RESULT 14				CC
AAW91072				CC
ID				CC
AAW91072 standard; protein; 1205 AA.				CC
AC				CC
XX				CC
DT				CC
07-JUN-1999 (first entry)				CC
XX				CC

Copyright (c) 1993 - 2005 Compugen Ltd.	GenCore version 5.1.6	WD-40 repeat prote probable membrane platelet-activatin beta transducin ho GTP-binding regula LIS-1 protein - hu	304	AGI837
OM protein - protein search, using sw model		S51445	310	320.5
Run on:	January 27, 2005, 18:30:10 ; Search time 52 Seconds (without alignments)	311.5	311.5	4.8
Title:	US-10-646-396-2	4.7	4.7	817
Perfect score:	6619	309	309	817
Sequence:	1 MDAKARNCLQHREALEKDI.....EKTYYTVTDNLGLYLIQTLLE 1248	307	307	4.7
Scoring table:	BLOSUM62	306	306	4.6
Gapop:	Gapop 10.0 , Gapext 0.5	304	304	4.6
Searched:	283416 seqs, 96216763 residues	302	302	4.6
Total number of hits satisfying chosen parameters:	283416	309	309	4.6
Minimum DB seq length: 0		309	309	304
Maximum DB seq length: 200000000		299	299	304
Post-processing: Minimum Match 0*		297.5	297.5	304
Maximum Match 100*		297.5	297.5	304
Listing first 45 summaries		297	297	304
Database :	PIR 79: 1: Pirl1: 2: Pir2: 3: Pir3: 4: pir4:	296.5	296.5	304
Scored No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.		294	294	304
SUMMARIES				
Result No.	Score	Query Match	Length	ID
				Description
1	6282	94.9	1194	2 T03818
2	732	11.1	1227	2 AB1810
3	728.5	11.0	1258	2 AI2155
4	691	10.4	1526	2 AC2239
5	677.5	10.2	1711	2 AD1842
6	672	10.2	1683	2 AF2071
7	643.5	9.7	1356	2 T18521
8	626	9.5	1693	2 S76086
9	614.5	9.3	934	2 AG1889
10	611.5	9.2	1551	2 AB2410
11	610	9.2	1708	2 AE1866
12	600.5	9.1	1189	2 AI2493
13	580.5	8.8	1189	2 AH2154
14	581.5	8.5	1747	2 AC1842
15	464.5	7.0	1329	2 AE1901
16	441.5	6.7	1101	2 T26919
17	423	6.4	2629	2 T322735
18	399.5	6.0	2629	2 T30987
19	396	6.0	1049	2 T42045
20	394	6.0	777	2 T41075
21	391	5.9	1191	2 S76414
22	385	5.8	677	2 AB1861
23	370	5.6	317	2 AG6032
24	369	5.6	786	2 AG2375
25	365	5.5	676	2 AH2195
26	355	5.4	876	2 TS1507
27	338	5.1	589	2 AG2400
28	326	4.9	559	2 AB2202
29	322.5	4.9	515	2 S19487

RESULT
AEI 810
WD-40

Sequence 16 Application US/09876667
 Patent No. US201010370A1
 GENERAL INFORMATION:
 APPLICANT: Hanzel, William J.
 TITLE OF INVENTION: APAF-1, AN ACTIVATOR OF C ASPASE-3
 NUMBER OF SEQUENCES: 16
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Merchant, Gould, Smith, Edell, Walter & Schmidt
 STREET: 3100 No. US202010370A1west Center, 90 South Seventh St
 CITY: Minneapolis
 STATE: MN
 ZIP: 55401
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/876, 667
 FILING DATE: 07-Jun-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/435, 115
 FILING DATE: <Unknown>
 APPLICATION NUMBER: 60/055, 258
 FILING DATE: 07-AUG-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Kettelberger, Ph. D., Denise M.
 REGISTRATION NUMBER: 33, 924
 REFERENCE/DOCKET NUMBER: 11669.6USU1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 612-332-5300
 TELEFAX: 612-332-9081
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1205 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 MOLECULE TYPE: protein
 FRAGMENT TYPE: internal
 FRAGMENT DESCRIPTION: SEQ ID NO: 16:
 / US-09-876-667-16

Query 181 GVKWVSVGKQDKSGLMLQNLCTRLDQDESFSQRUPLNIEAKDRILMRLKHPRSSL 240
 Query 241 ILDDVVDSWVLKAQFDQCCQILLTRDKSVTDSMGPXVYVPESSLGKEKGELSLFVN 300
 Database 241 ILDDVVDSWVLKAQFDQCCQILLTRDKSVTDSMGPXVYVPESSLGKEKGELSLFVN 300
 Query 301 MKKADLPQAHSIIKECKGSPLVSYLSIGALLDDEPRWEYKLQLQNKOFKRKSSYD 360
 Database 301 MKKADLPQAHSIIKECKGSPLVSYLSIGALLDDEPRWEYKLQLQNKOFKRKSSYD 360
 Query 361 YEALDEAMSISYEMIREDIMDYYTDLSDLQDKVYKPTVCLIDMDMETEEDILQEVFN 420
 Database 361 YEALDEAMSISYEMIREDIMDYYTDLSDLQDKVYKPTVCLIDMDMETEEDILQEVFN 420
 Query 421 KSLIFCDRNGKSFRYLHDIQVDFLTENCSQDQDHKKITQFORVHQPHLSPDODC 480
 Database 421 KSLIFCDRNGKSFRYLHDIQVDFLTENCSQDQDHKKITQFORVHQPHLSPDODC 480
 Query 481 MYWNFLAYMASAKHKECALMFSLWIKAKTELGVPAHLIPEFVYRHLDEKCAV 540
 Database 481 MYWNFLAYMASAKHKECALMFSLWIKAKTELGVPAHLIPEFVYRHLDEKCAV 540
 Query 541 SENQFEPISLNLGHGRQPPNITQVLGICPEPTESEYVQQAKLQKOEVDNGMLYLEWINK 600
 Database 541 SENQFEPISLNLGHGRQPPNITQVLGICPEPTESEYVQQAKLQKOEVDNGMLYLEWINK 600
 Query 601 KNITNLRLVYRPHRTDAVTAFCSEDGORIASCGADKTLQVKATGEKLLRKADEV 660
 Database 601 KNITNLRLVYRPHRTDAVTAFCSEDGORIASCGADKTLQVKATGEKLLRKADEV 660
 Query 661 LCCAFTSDDRFLATCSVDKVKTWNSMTGELVHTDDEHSQVNCHFTNSHLLATGS 720
 Database 661 LCCAFTSDDRFLATCSVDKVKTWNSMTGELVHTDDEHSQVNCHFTNSHLLATGS 720
 Query 721 SDQFLKLWDLNQKECRNTMEHGHTNSVNHCRSPDDKLASCADGTLKLWDTANSWERK 780
 Database 721 SDQFLKLWDLNQKECRNTMEHGHTNSVNHCRSPDDKLASCADGTLKLWDTANSWERK 780
 Query 781 INYKQFFPLNEDPQEMETVYKCCSWASDAGARIMYAKNKLFDLINTSGLGLEHTGH 840
 Database 781 INYKQFFPLNEDPQEMETVYKCCSWASDAGARIMYAKNKLFDLINTSGLGLEHTGH 840
 Query 841 STIQYCDPSQPNLHLAVALSQCYCVELNTDSKVAQHLSVHGMFSQDGSSLTS 900
 Database 841 STIQYCDPSQPNLHLAVALSQCYCVELNTDSKVAQHLSVHGMFSQDGSSLTS 900
 Query 901 SDQDTIRLWETAKVCKNSAMVLMKOEVDYVPEQEENVMVLAHDIBRLQLINGRQDYL 960
 Database 901 SDQDTIRLWETAKVCKNSAMVLMKOEVDYVPEQEENVMVLAHDIBRLQLINGRQDYL 960
 Query 961 EAQVSCCCLSPHLOXTAFGENGAEILEYVNTRFQSFRQHKKTWHIQFADEXTLIS 1020
 Database 961 EAQVSCCCLSPHLOXTAFGENGAEILEYVNTRFQSFRQHKKTWHIQFADEXTLIS 1020
 Query 1021 SSDDAETQVNWNQWDLKCIFRGHOETVQDFRULKNSRLLSWSFQGTVKWNLTGNKEKD 1080
 Database 1021 SSDDAETQVNWNQWDLKCIFRGHOETVQDFRULKNSRLLSWSFQGTVKWNLTGNKEKD 1080
 Query 1081 FVCHQGTIVLSCSIDATKESPSADTAKWMSFDLPLPHELAGINGCVRSAFSVYST 1140
 Database 1081 FVCHQGTIVLSCSIDATKESPSADTAKWMSFDLPLPHELAGINGCVRSAFSVYST 1140
 Query 1141 LIATGDDNGEIRINNVNSNGELLHCAPLSERGAATHGGNYTDLCPDKMULISAGGYIK 1200
 Database 1141 LIATGDDNGEIRINNVNSNGELLHCAPLSERGAATHGGNYTDLCPDKMULISAGGYIK 1200
 Query 1201 WNNVTGBESSQFTYGTGTLKICHVSPDFKTYVTDNLGLYLTQITLE 1248
 Database 1201 WNNVTGBESSQFTYGTGTLKICHVSPDFKTYVTDNLGLYLTQITLE 1248
 Query 1241 ILDDVVDSWVLKAQFDQCCQILLTRDKSVTDSMGPXVYVPESSLGKEKGELSLFVN 300
 Database 1241 ILDDVVDSWVLKAQFDQCCQILLTRDKSVTDSMGPXVYVPESSLGKEKGELSLFVN 300
 Query 301 MKKADLPQAHSIIKECKGSPLVSYLSIGALLDDEPRWEYKLQLQNKOFKRKSSYD 360
 Database 301 MKKADLPQAHSIIKECKGSPLVSYLSIGALLDDEPRWEYKLQLQNKOFKRKSSYD 360

RESULT 2
 US-09-876-667-16

CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/876,667
FILING DATE: 0-Jun-2001

PRIOR APPLICATION DATA:
CLASSIFICATION: <Unknown>
APPLICATION NUMBER: 09/435,115
FILING DATE: <Unknown>
APPLICATION NUMBER: 60/055,258
FILING DATE: 0-AUG-1997

ATTORNEY/AGENT INFORMATION:
NAME: Kettlerberger, Ph.D., Denise M
REGISTRATION NUMBER: 33,024
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1194 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-876-667-2

Query Match 94.9%; Score 6282; DB 9; Length 1194;
Best Local Similarity 95.7%; Pred. No. 0; Mis matches 0; Indels 54; Gaps 2;

Matches 1194; Conservative 1 MDAKARNCLQHREALEKIKTSYIMDAMISDGFTLISEEKVNNEPTQQRAAMLKMI 60
1 MDAKARNCLQHREALEKIKTSYIMDAMISDGFTLISEEKVNNEPTQQRAAMLKMI 60

61 LKKNDSDYVSFYNALIHEGYKDLMHLHDGIPWVSSSGRDSVSITSYRTVLCEGGVP 120
61 LKKNDSDYVSFYNALIHEGYKDLMHLHDGIPWVSSSGRDSVSITSYRTVLCEGGVP 109

Db 121 QRPVVFVTRKLYNAIQQLSKLRKEPGWVTTGAGCGKSVLAAVARDHSLLRGCFPG 180

62 110 QRPVVFVTRKLYNAIQQLSKLRKEPGWVTTGAGCGKSVLAAVARDHSLLRGCFPG 169

Db 170 GHVNTSVGKQDKSGMLQNLCTPDLQDQESFSQPLNIEAKRLRILMRKPRSL 229

Db 241 ILDDWDWSWVTKAFSQCLLITRDKSVDTSWICSPKYPVESSLGKEKGLEIISLFWN 300
230 ILDDWDWSWVTKAFSQCLLITRDKSVDTSWICSPKYPVESSLGKEKGLEIISLFWN 289

Db 301 MKKAQPEAQHSITIMECKGSPLVYSLIGALLRDFFPNRWEYLKOLQNKOPKRIRKSSYD 360
290 MKKAQPEAQHSITIMECKGSPLVWIGAQLRDFNRWEYTLKQJNQKPKRIRKSSYD 349

361 YEALDEAMSISVEMREDIKDYTTSLSLOKDVKPTKVLCILNMETEEVEDILQEFVN 420
350 YEALDEAMSISVEMREDIKDYTTSLSLOKDVKPTKVLCILNMETEEVEDILQEFVN 409

421 KSLLFCDRNEKSFRYTLHDLOQDFTEKNSQOLQHRCITQFORYHQHTLSSDQEDC 480
410 KSLLFCDRNEKSFRYTLHDLOQDFTEKNSQOLQHRCITQFORYHQHTLSSDQEDC 469

RESULT 3
Sequence 2, Application US/09876667
Patent No. US20020107370A1
GENERAL INFORMATION:
Applicant: Henzel, William J.
Title of Invention: APAP-1, AN ACTIVATOR OF C ASPASE-3
Number of Sequences: 16
Correspondence Address:
Address: Merchant, Gould, Smith, Edelli, Walter & Schmidt
Street: 3100 No. US20020107370Alwest Center, 90 South Seventh St

RESULT 4
US-10-141-618-10
Sequence 10, Application US/10141618
Publication No. US20030165887A1
GENERAL INFORMATION:
APPLICANT: Reed, John C.
TITLE OF INVENTION: Methods For Determining the Prognosis
FILE REFERENCE: P-LJ 5254
CURRENT FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: US 60/289, 233
PRIOR FILING DATE: 2001-05-07
PRIOR APPLICATION NUMBER: US 60/355, 934
PRIOR FILING DATE: 2002-02-12
PRIOR APPLICATION NUMBER: US 09/388, 221
PRIOR FILING DATE: 1999-09-01
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 10

Qy 481 MYWWNFLAYHMASAKOHKEKCALMFLDKWIKAKTTELVGPALIHFVEYRHLDEKDCAV 540
Db 470 MYWWNFLAYHMASAKOHKEKCALMFLDKWIKAKTTELVGPALIHFVEYRHLDEKDCAV 529
Qy 541 SENFOEFLSINGHLLGRQPNNVOLGLCPEPETSEYQQAKLQAQKYEVDNGMLYLEWINK 600
Db 530 SENFOEFLSINGHLLGRQPNNVOLGLCPEPETSEYQQAKLQAQKYEVDNGMLYLEWINK 589
Qy 531 KNITNLSPRLVVRPHDTAVHACFEDGDRIASGADKTLOVKAEKGKLLEKAHDEV 60
Db 590 KNITNLSPRLVVRPHDTAVHACFEDGDRIASGADKTLOVKAEKGKLLEKAHDEV 649
Qy 661 LCCAFSTDDRFATCSVDKVKVTKNSMTGEVLVTHDEHSEVNCCHFTNSHILLATGS 720
Db 650 LCCAFSTDDRFATCSVDKVKVTKNSMTGEVLVTHDEHSEVNCCHFTNSHILLATGS 709
Qy 721 SDCEPLKNDLNOKECENTMFGHTNSVHCRFSPDDKLASCASAGTTLKWDTSANERKS 780
Db 710 SDCEPLKNDLNOKECENTMFGHTNSVHCRFSPDDKLASCASAGTTLKWDTSANERKS 769
Qy 781 INVQOFFNLNEDPQDMEVYKCCSWASDAGARIMVAAKNKFELDFTSGLGEIHTGHH 840
Db 770 INVQOFFNLNEDPQDMEVYKCCSWASDAGARIMVAAKNKF----- 811
Qy 841 STIQYCDPSQNPHLAVLSSQCYCVELNTDSRSKVADCGRHLSWVHGYMFSPDGSSFLTS 900
Db 812 -----LNTDSRSKVADCGRHLSWVHGYMFSPDGSSFLTS 846
Qy 901 SDQDTIRIWETKVKVNSAMLKQEVDPVDFQENEVNVLAYDHIRRLONGTGQDYL 960
Db 847 SDQDTIRIWETKVKVNSAMLKQEVDPVDFQENEVNVLAYDHIRRLONGTGQDYL 906
Qy 961 EAQVSCCCLSPHQTAFGENGCAIEELVNNTIROSQRHQCKTWNHIOFADTEKTLIS 1020
Db 907 EAQVSCCCLSPHQTAFGENGCAIEELVNNTIROSQRHQCKTWNHIOFADTEKTLIS 966
Qy 1021 SSDDAETQWWNQLDKCIFLRGHOETVDFRLLKNSRLSWSFDGTWVUNNTITGNKEKD 1080
Db 967 SSDDAETQWWNQLDKCIFLRGHSETVDFRLLKNSRLSWSFDGTWVUNNTITGNKEKD 1026
Qy 1081 FVCHQGTVLSCDISDATAKSSTADKTAKTWSFDLILPHELGHNGCYRCASFVSDST 1140
Db 1027 FVCHQGTVLSCDISDATAKSSTADKTAKTWSFDLILPHELGHNGCYRCASFVSDST 1086
Qy 1141 LLATGDONGERIWVNSGELLHICAPUSEGAATGGWTDLCFSPOGMISAGYIK 1200
Db 1087 LLATGDONGERIWVNSGELLHICAPUSEGAATGGWTDLCFSPOGMISAGYIK 1146
Qy 1201 WNWNTUGERSQTYINGTNLKKITHUSDPRKTYTUDNLGLYLQOTL 1248
Db 1147 WNWVTGBSSQFYTINGTNLKKITHUSDPRKTYTUDNLGLYLQOTL 1144
Qy LENGTH: 11.94
Db TYPE: PRT
Organism: Homo sapiens
US-10-141-618-10

Query Match 94.9%; Score 6282; DB 14; Length 11.94;
Best Local Similarity 95.7%; No. 0; Mismatches 0; Indels 54; Gaps 2;
Matches 11.94; Conservative 0; MisMatches 0; Indels 54; Gaps 2;

Qy 1 MDAKARNCLLQHREALFKDITKTSYIMDHMISGFLTISEEKVNRNEPTOQRAMLKIMI 60
Db 1 MDAKARNCLLQHREALFKDITKTSYIMDHMISGFLTISEEKVNRNEPTOQRAMLKIMI 60
Qy 61 LKCONDTSVSYFNALLHEGTDLALLHDGIPVUSSSGKDSVSCTSYRTLCEGCPV 120
Db 61 LKCONDTSVSYFNALLHEGTDLALLHDGIPVUSSSGKDSVSCTSYRTLCEGCPV 109
Qy 121 QRPVVFUTRKLVNUAQQLSKLKGEPGWVTHGMAGCGRSLVLANBAVTDHSLEGCFFG 180
Db 110 QRPVVFUTRKLVNUAQQLSKLKGEPGWVTHGMAGCGRSLVLANBAVTDHSLEGCFFG 169
Qy 181 GHRRVSVKQDGSGLMKLONLCTRLDODESSQRPLNTEAKDLRTRMLKHPSSL 240
Db 170 GHRRVSVKQDGSGLMKLONLCTRLDODESSQRPLNTEAKDLRTRMLKHPSSL 229
Qy 241 ILDDWWDWVLAKFDSQCQILITTRDKSVTDSVGMGPKVYYVESSLGKEKGKLTSIFVN 300
Db 230 ILDDWWDWVLAKFDSQCQILITTRDKSVTDSVGMGPKVYYVESSLGKEKGKLTSIFVN 289
Qy 301 MKCADLPQEASLIRECKGSPLVYSLIGALLRDFPNRWEYTLKOLQNKOFKRTRKSSYD 360
Db 290 MKCADLPQEASLIRECKGSPLVYSLIGALLRDFPNRWEYTLKOLQNKOFKRTRKSSYD 349
Qy 361 YEALDEAMSISVEMREDIKYXTDLSLQDQKVKPVLILWMETEEVEDLQEFPV 420
Db 350 YEALDEAMSISVEMREDIKYXTDLSLQDQKVKPVLILWMETEEVEDLQEFPV 409
Qy 421 KSLIFCDRNGSFRTYFLHLDQDFTERKNCSQDOLHKKLTQFORYHOHTSPDQEDC 480
Db 410 KSLIFCDRNGSFRTYFLHLDQDFTERKNCSQDOLHKKLTQFORYHOHTSPDQEDC 469
Qy 481 MYWWNFLAYHMASAKOHKEKCALMFLDKWIKAKTTELVGPALIHFVEYRHLDEKDCAV 540
Db 470 MYWWNFLAYHMASAKOHKEKCALMFLDKWIKAKTTELVGPALIHFVEYRHLDEKDCAV 529
Qy 541 SENFOBTSLSNHLGRQPPNTVQGLCEPSETSEYQQAKLQAQEVNDGMYLEWINK 600
Db 530 SENFOBTSLSNHLGRQPPNTVQGLCEPSETSEYQQAKLQAQEVNDGMYLEWINK 589
Qy 601 KNTNLSPRLVPHDFTAVHACFEDGRIAAGXKLTQFRTGKLLKLEKAHDEV 660
Db 590 KNTNLSPRLVPHDFTAVHACFEDGRIAAGXKLTQFRTGKLLKLEKAHDEV 649
Qy 661 LCCAFSTDIDRFTATCSVDKKVTKNSMGTFLHSDHSONVCHFTNSHILLATGS 720
Db 650 LCCAFSTDIDRFTATCSVDKKVTKNSMGTFLHSDHSONVCHFTNSHILLATGS 709
Qy 721 SDCEPLKNDLNOKECRNTMFGHTNSVHCRFSPDDKLASCADGTLKWDTSANERKS 780
Db 710 SDCEPLKNDLNOKECRNTMFGHTNSVHCRFSPDDKLASCADGTLKWDTSANERKS 769
Qy 781 INVQOFFNLNEDPQDMEVYKCCSWASDGAIRIMVAKNCFLPDHTSGLJBHFGHH 840
Db 770 INVQOFFNLNEDPQDMEVYKCCSWASDGAIRIMVAKNCFLPDHTSGLJBHFGHH 811
Qy 841 STIQYCDPSQNHLAVLSSQCYCVELNTDSRSKVADCGRHLSWVHGYMFSPGSSFLTS 900
Db 812 -----LNTDSRSKVADCGRHLSWVHGYMFSPGSSFLTS 846
Qy 901 SDDOTIWLWETKVKVNSGELLHICAPUSEGAATGGWTDLCFSPOGMISAGYIK 960
Db 847 SDDOTIWLWETKVKVNSGELLHICAPUSEGAATGGWTDLCFSPOGMISAGYIK 906

RESULT 5

US-10-112-944-273

; Sequence 273, Application US/10112944

; Publication No. US20040048249A1

; GENERAL INFORMATION:

; APPLICANT: Tang, Y. Tom

; APPLICANT: Yang, Yonghong

; APPLICANT: Weng, Gezhi

; APPLICANT: Zhang, Jie

; APPLICANT: Ren, Feiyun

; APPLICANT: Xue, Aidong J.

; APPLICANT: Wang, Jian-Rui

; APPLICANT: Wehrman, Tom

; APPLICANT: Ghosh, Malabika

; APPLICANT: Wang, Dunrui

; APPLICANT: Zhao, Qing A.

; APPLICANT: Wang, Zhiwei

; TITLE OF INVENTION: No. US20040048249A1el Nucleic Acids and Secreted Polypeptides

; FILE REFERENCE: 805A

; CURRENT APPLICATION NUMBER: US/10/112,944

; CURRENT FILING DATE: 2002-03-28

; PRIOR APPLICATION NUMBER: US 09/488,725

; PRIOR FILING DATE: 2000-01-21

; PRIOR APPLICATION NUMBER: US 09/491,404

; PRIOR FILING DATE: 2000-01-25

; PRIOR APPLICATION NUMBER: US 09/496,914

; PRIOR FILING DATE: 2000-02-03

; PRIOR APPLICATION NUMBER: US 09/515,126

; PRIOR FILING DATE: 2000-02-28

; PRIOR APPLICATION NUMBER: US 09/519,705

; PRIOR FILING DATE: 2000-03-07

; PRIOR APPLICATION NUMBER: US 09/510,217

; PRIOR FILING DATE: 2000-03-31

; PRIOR APPLICATION NUMBER: US 09/552,929

; PRIOR FILING DATE: 2000-04-18

; PRIOR APPLICATION NUMBER: US 09/577,408

; PRIOR FILING DATE: 2000-05-18

; NUMBER OF SEQ ID NOS: 924

; SOFTWARE: pt_FL_genes Version 5.0

; SEQ ID NO: 273

; LENGTH: 1199

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-112-944-273

Query Match 90.7%; Score 6003.5; DB 15; Length 1199;

Best Local Similarity 89.2%; Pred. No. 0;

Matches 1154; Conservative 0; Mismatches 0; Indels 139; Gaps 5;

Qy 1 MDAAKNCNLQOHLREALEDKIKTSTMIDMISDQFLTSSEEVNRNPTQQPAAAMIKWI 60

RESULT 6
US-10-112-944-272

/ Sequence 272, Application US/10/112944

/ Publication No. US20040048249A1

/ GENERAL INFORMATION:

/ APPLICANT: Tang, Y. Tom

/ APPLICANT: Yang, Yongzhong

/ APPLICANT: Wang, Gezhi

/ APPLICANT: Zhang, Jie

/ APPLICANT: Ren, Feiyan

/ APPLICANT: Xue, Aidiang, J.

/ APPLICANT: Wang, Jian-Rui

/ APPLICANT: Wehrman, Tom

/ APPLICANT: Ghosh, Malabika

/ APPLICANT: Wang, Dunrui

/ APPLICANT: Zhao, Qing A.

/ APPLICANT: Wang, Zhivei

/ TITLE OF INVENTION: Secreted Polypeptides

/ FILE REFERENCE: 805A

CURRENT APPLICATION NUMBER: US/10/112,944

CURRENT FILING DATE: 2002-03-28

PRIOR APPLICATION NUMBER: US 09/488,725

PRIOR FILING DATE: 2000-01-21

PRIOR APPLICATION NUMBER: US 09/431,404

PRIOR FILING DATE: 2000-01-25

PRIOR APPLICATION NUMBER: US 09/496,914

PRIOR FILING DATE: 2000-02-03

PRIOR APPLICATION NUMBER: US 09/515,126

PRIOR FILING DATE: 2000-02-28

PRIOR APPLICATION NUMBER: US 09/519,705

PRIOR FILING DATE: 2000-03-07

PRIOR APPLICATION NUMBER: US 09/540,217

PRIOR FILING DATE: 2000-03-31

PRIOR APPLICATION NUMBER: US 09/555,929

PRIOR FILING DATE: 2000-04-18

PRIOR APPLICATION NUMBER: US 09/577,408

PRIOR FILING DATE: 2000-05-18

NUMBER OF SEQ ID NOS: 924

SOFTWARE: pt_Fl_Genes Version 5.0

SEQ ID NO: 272

LENGTH: 1526

TYPE: PT

ORGANISM: Homo sapiens

US-10-112-944-272

Query Match 89.6%; Score 5933.5; DB 15; Length 1526;

Best Local Similarity 89.1%; Pred. No. 0; Mismatches 0; Indels 139; Gaps 5;

Matches 1141; Conservative 0; Gaps 5;

Qy 14 EALEKDIKTKSTIMDAMISGFLTISEEKRVNEPTQQRAALIIMLKIKNDSTVSYN 73

Db 341 EALEKDIKTKSTIMDAMISGFLTISEEKRVNEPTQQRAALIIMLKIKNDSTVSYN 400

Qy 74 ALLHEGYKDIAALLHDGIPWVSSSSGRDSVSCITSVRTUCEGGFQPORVVFTRKLV 133

Db 401 ALLHEGYKDIAALLHDGIPWVSSSSGRDSVSCITSVRTUCEGGFQPORVVFTRKLV 449

Qy 134 NAIQOKLUSKLKGEPWTWIGMAGCGKSVLAAEYRDHSILLEGCFPGGVHWSVGKQDKS 193

Db 450 NAIQOKLUSKLKGEPWTWIGMAGCGKSVLAAEYRDHSILLEGCFPGGVHWSVGKQDKS 509

Qy 194 GLMLKQLQNLCLTRLDQDESFSQRQLNITEAKDLRILMRKPRSLIILDDVDSWVTKA 253

Db 510 GLMLKQLQNLCLTRLDQDBSFQRPLNITEAKDLRILMRKPRSLIILDDVDSWVTKA 569

Qy 254 FDSCQCOLLITTRDKSYTDMSGPKVYVPESSSIGKEKGLTLTSIFVNMMKADLPREOAHSI 313

Db 570 FDSCQCOLLITTRDKSYTDMSGPKVYVPESSSIGKEKGLTLTSIFVNMMKADLPREOAHSI 629

Qy 314 IKBCKGSPLVSLGALLRDPNWEYXKOLQONKOPKRTRKSSSYDEALDBAMSISVE 373

Db 630 IKBCK- ---VSIGLLRDPNWEYXKOLQONKOPKRTRKSSSYDEALDBAMSISVE 684

Qy 374 MLREDDIDYYDTDLIQLQDVVKPKVLCILWMETEEVEDILQEFVNKSLLFCDRNGKSF 433

Db 685 MLREDDIDYYDTDLIQLQDVVKPKV-----709

Qy 434 RYVYLHDLQVDFTLTERNCNSQLQDLHKC1LTORQRYHOPHTLSPODQEDCMYKWNPLAYHMAS 493

Db 710 -----DLRKCTTIOFRYHQHTLSPQEDCMYKWNPLAYMAS 748

Qy 494 AKMHKELCALMFSLWDWKATKELVGPANLHFVEVRLHILDEKDAVSENFOEFLSLNGH 553

Db 749 AKMHKELCALMFSLDKTAKELVGPANLHFVEVRLHILDEK-----791

Qy 554 LLGRQPFPNIVOLGLCEPETSVEYQAKLQAOKEVONGMLYLEWINKNNTNLSRLVVRP 613

Db 792 ----PPFNIVOLGLCEPETSVEYQAKLQAOKEVONGMLYLEWINKNNTNLSRLVVRP 846

Qy 614 HTDAYHACFSEDGORIASGADKTLO-----640

Db 847 HTDAYHACFSEDGORIASGADKTLO-----640

Qy 641 -----VETAEETGKELVPAETGKELIKAHEDEVLCCAFSTDPRFATCSVDKKVTKWISMT 688

Db 907 VLLGDLSGPPLAVKATGKELIKAHEDEVLCCAFSTDPRFATCSVDKKVTKWISMT 966

Qy 689 GELVHTDEHSEQVNCCHTFTNSHLLJLATSDFCPFLKUDLNOKECRNTMPGHTNSVNH 748

Db 967 GELVHTDEHSEQVNCCHTFTNSHLLJLATSDFCPFLKUDLNOKECRNTMPGHTNSVNH 1026

Qy 749 CRFSPDDKLASCASDGTKLWDATSANERKSINVQFFNLQEDQEMEVTKCCWSA 808

Db 1027 CRFSPDDKLASCASDGTKLWDATSANERKSINVQFFNLQEDQEMEVTKCCWSA 1086

Qy 809 DGARIMVAAKKNIKFLDITSGLGEIHTGHISTIQYCDESPONHLAVALSQXYCBLWN 868

Db 1087 DGARIMVAAKKNIKFLDITSGLGEIHTGHISTIQYCDESPONHLAVALSQXYCBLWN 1146

Qy 869 TDSRSKVADCRGHLSSVHGGMFSPDGSSFLTSSDDOTIRLWEETKVKVNSAVNLKOEVVDV 928

Db 1147 TDSRSKVADCRGHLSSVHGGMFSPDGSSFLTSSDDQITRLWEETKVKVNSAVNLKOEVVDV 1206

Qy 929 VEQENVMVLAVIDHRRQLQINGRTGQDYLTEAQVSCCCUSPHQYTAFGDNGATEIL 988

Db 1207 VEQENVMVLAVIDHRRQLQINGRTGQDYLTEAQVSCCCUSPHQYTAFGDNGATEIL 1266

Qy 989 ELYNNR1FSPRQHCKTVWHIQTADEETLISSSDAEIQWNVNQLDKCIIFLGHQETVK 1048

Db 1267 ELYNNR1FSPRQHCKTVWHIQTADEETLSSSDAEIQWNVNQLDKCIIFLGHQETVK 1326

Qy 1049 DFLIKNSRLSWSFDCGTVKVNNTGENKEKDFCHQTVLSCDISHDATAFSTSADKT 1108

Db 1327 DFLIKNSRLSWSFDCGTVKVNNTGENKEKDFCHQTVLSCDISHDATAFSTSADKT 1386

Qy 1109 AKWSFDLPLIHLERGNGCVRCSAFSYDSTLAFGDDNGEIRIWNVNGELHLHCAPL 1168

Db 1387 AKWSFDLPLIHLERGNGCVRSAFVDSLILAQDDNGEIRIWNVNGELHLHCAPL 1446

Qy 1169 SEEGAATHGGWVTDLCSFDGKMLISAGGYIWVNNTVTGBSSQTYTNGTNLKTHYSPD 1228

RESULT 7

Db 1447 SEEGAATHGGRTDLCLFSPDGKMLISAGGYIKWWVVVTGESSQTFYTNGLKTHVSSPD 1506 ; SEQ ID NO 31
 Qy 1229 FKTYYTVNDLNLGILYIQLTE 1248 ; LENGTH: 308
 Db 1507 FKTYYTVNDLNLGILYIQLTE 1526 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-002-974-31

Query Match 24.0%; Score 1589; DB 13; Length 308;
 Best Local Similarity 100.0%; Pred. No. 1.8e-118;
 Matches 308; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 123 PVVFTRKLVNAIQQLSKLGEGWTHGMAGCGKSYLAAEAVRDHSLEGGPGGV 182
 Db 1 PVVFTRKLVNAIQQLSKLGEGWTHGMAGCGKSYLAAEAVRDHSLEGGPGGV 60

Query Match 24.0%; Score 1589; DB 13; Length 308;
 Best Local Similarity 100.0%; Pred. No. 1.8e-118;
 Matches 308; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 183 HWVSYGKDKDGSGLMQLQNLCTRLLQDEFSQRQLNIEAKDRIRLMLRKHPSLLIL 242
 Db 61 HWVSYGKDKDGSGLMQLQNLCTRLLQDEFSQRQLNIEAKDRIRLMLRKHPSLLIL 120

Query Match 24.0%; Score 1589; DB 13; Length 308;
 Best Local Similarity 100.0%; Pred. No. 1.8e-118;
 Matches 308; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 243 DDWWDWSWVLKAQFDSQCILLTRDKSVTDSMGPCKVVPYESSLGKEKGLEILSIFVNMK 302
 Db 121 DDWWDWSWVLKAQFDSQCILLTRDKSVTDSMGPCKVVPYESSLGKEKGLEILSIFVNMK 180

Query Match 24.0%; Score 1589; DB 13; Length 308;
 Best Local Similarity 100.0%; Pred. No. 1.8e-118;
 Matches 308; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 303 KADLPEQAHASLTIKECKGSPLVVSLIGALRDFPNWEYVYLQLOQNQFKRIRKSSSYDYE 362
 Db 181 KADLPEQAHASLTIKECKGSPLVVSLIGALRDFPNWEYVYLQLOQNQFKRIRKSSSYDYE 240

Query Match 24.0%; Score 1589; DB 13; Length 308;
 Best Local Similarity 100.0%; Pred. No. 1.8e-118;
 Matches 308; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 363 ALDEAMSISEVMLREDIKDYTDLSLQDVVKVPKVLCILWDMTEEVEDILOQEVNKS 422
 Db 241 ALDEAMSISEVMLREDIKDYTDLSLQDVVKVPKVLCILWDMTEEVEDILOQEVNKS 300

RESULT 9

US-10-314-506-31

Sequence 31, Application US/10314506
 Publication No. US20030175162A1

; GENERAL INFORMATION:
 ; APPLICANT: Nunez, Gabriel
 ; INVENTOR: Inohara, Naohiro
 ; APPLICANT: Ogura, Yasunori
 ; TITLE OF INVENTION: Modulators of NOD2 Signaling
 ; FILE REFERENCE: US-06984
 ; CURRENT FILING DATE: 2002-12-09
 ; PRIOR APPLICATION NUMBER: 10,014,269
 ; PRIOR FILING DATE: 2001-10-26
 ; PRIOR APPLICATION NUMBER: 60/244,289
 ; PRIOR FILING DATE: 2000-10-30
 ; NUMBER OF SEQ ID NOS: 62
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 31
 ; LENGTH: 308
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-314-506-31

Query Match 24.0%; Score 1589; DB 14; Length 308;
 Best Local Similarity 100.0%; Pred. No. 1.8e-118;
 Matches 308; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 123 PVVFTRKLVNAIQQLSKLGEGWTHGMAGCGKSYLAAEAVRDHSLEGGPGGV 182
 Db 1 PVVFTRKLVNAIQQLSKLGEGWTHGMAGCGKSYLAAEAVRDHSLEGGPGGV 60

Query Match 24.0%; Score 1589; DB 13; Length 308;
 Best Local Similarity 100.0%; Pred. No. 1.8e-118;
 Matches 308; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 183 HWVSYGKDKDGSGLMQLQNLCTRLLQDEFSQRQLNIEAKDRIRLMLRKHPSLLIL 242
 Db 61 HWVSYGKDKDGSGLMQLQNLCTRLLQDEFSQRQLNIEAKDRIRLMLRKHPSLLIL 120

Query Match 24.0%; Score 1589; DB 13; Length 308;
 Best Local Similarity 100.0%; Pred. No. 1.8e-118;
 Matches 308; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 243 DDWWDWSWVLKAQFDSQCILLTRDKSVTDSMGPCKVVPYESSLGKEKGLEILSIFVNMK 302
 Db 301 LLFCDRNG 308

RESULT 8

US-10-002-974-31

Sequence 31, Application US/10002974
 Publication No. US2002197616A1

; GENERAL INFORMATION:
 ; APPLICANT: Nunez, Gabriel
 ; INVENTOR: Inohara, Naohiro
 ; APPLICANT: Cho, Judy
 ; APPLICANT: Nicola, Dan L
 ; APPLICANT: Bonen, Denise
 ; TITLE OF INVENTION: NOD2 Nucleic Acids and Proteins
 ; FILE REFERENCE: US-06646
 ; CURRENT FILING DATE: 2001-10-26
 ; NUMBER OF SEQ ID NOS: 99
 ; SOFTWARE: PatentIn version 3.1

Db 121. DDVWDSWVTKAFDSQCQILLTRDKSVTDSVNGPKVVPVSSLGKEKGLEILSFLVNMK 180
 ; CURRENT APPLICATION NUMBER: US/10/369,493
 ; CURRENT FILING DATE: 2003-02-08
 ; PRIOR APPLICATION NUMBER: US 60/360,039
 ; PRIORITY FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO: 12913
 ; LENGTH: 529
 ; TYPE: PRT
 ; ORGANISM: Aspergillus nidulans
 us-10-369-493-12913

Query Match 10.7%; Score: 711; DB: 14; Length: 529;
 Best Local Similarity 29.0%; Pred. No. 1e-47;
 Matches 183; Conservative 93; Mismatches 242; Indels 112; Gaps 11;

Qy 614 HTPAVYHACFSPDGORIASCGADTLOVEFKATHEDEVLUCAFTDDERIA 673
 Db 4 HLGEVESVVFSPDGKOLVSSYSDTVK1WDPTGELLQNDQHSCTVSLAFLPDGKLLA 63

Qy 674 TCSVDKVKVIRNSMTOLBVTYDDBHSEOVNCCHFTNSSHILLATGSSDPLFLWDLINKQ 733
 Db 64 SGSYDNTTIDLNSPDTGBLQFEGPHPAIWVAFAPDGKB - LASASDSTTIKWLDTAG 121

Qy 734 ECANTMFGHTSYNHCRFSDDKLASSADGTKLKDWTASANERKSINVKQFLNLEDP 793
 Db 122 ELQQTLDHSQEVRSVTAFSDDGKLLASSDLTTIKWNPATGELQSL --- 169

Qy 794 QEDMEVYKCCSWASDARTMVA - KRNIFLFDIHTSGHLGEINTGHSHTOYCDFSPOV 852
 Db 170 -EGRSGWKSTAFSPGKCKLASSBKNTVKLNPATGELLOTL GHSSOVSRSVAFSPDG 227

Qy 853 HLAVVALSQYCYELWNTDSRSKVADCRGHLSPVHGMSPDGSSFLTSDDQTRILWTK 912
 Db 228 KQLAQSSSDTITKLANKSTIGCBLQQTFKHDLMIRAYATAFSPDGKHLVSGSDDNNTIKLN -- 284

Qy 913 KVCKNSAVMLRQEVDVVFQENETRVLAVDHIRQLLINGTGQDILTEAQVSCCLSPH 972
 Db 285 ----- 284

Qy 973 LQYIAFGDENGAIIELYNNRIFOSRFQHKKTMHQFTADEXKLISSSDABIQWN- 1031
 Db 285 ----- DLA7SBLQSLSEDHSVHAVAIFSPDQKLASSDLTIKWLDS 328

Qy 1032 -WOLDKCIFLRLHQETVKDFRLKNSRL-SWSFDGTVKWNNTIGNEKEKDVFCHQSTV 1088
 Db 329 ATGELQRT -LEGHSQGURSVTFSPDGKLLANSYDGTIKWNPITGELQQTJGRSDWV 386

Qy 1089 LSCDISHADTSSTSADTAKWFSFDLJLPHELQHGNGVRCSAFSYDSTILATGDDN 1148
 Db 387 DSVAFSPDGKQKOLASGYDYSTIKWDSATGELLQTLGHSDRIOSTVFSPDGKLLASGPTN 446

Qy 1149 GEIRIAVNSGELLHICAPISSEGAAHTGGWVTDLCPSPDCMLISA - GCYI KWNWVVT 1206
 Db 447 KPARFWDATGPQLIF ---EG -- HSKWVBSVAFSPDGKLLASSYGETIKLWDEPT 498

Qy 1207 GBSQOTYTNGLKTHYSPDFTKTYVD 1236
 Db 499 GELQTLNDPDESAGSVAFSPDGNLASVD 528

RESULT 12
 US-10-369-493-20185
 Sequence 12913, Application US/10369493
 ; Publication No. US2003023367/5A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Chen, Xianlieng
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 ; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
 ; FILE REFERENCE: 38-10(52052)B

CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIORITY NUMBER: US 60/360,039
; PRIORITY FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO: 20185
; LENGTH: 610
; TYPE: PRT
; ORGANISM: No. US20030233675A1toc punctiforme
; US-10-369-493-20242

Query Match 10.4%; Score 690.5; DB 14; Length 610;
Best Local Similarity 28.7%; Pred. No. 5.7e-46; Matches 187; Conservative 106; Mismatches 273; Indels 85; Gaps 14;

Qy 614 HTDAYTHACFSEDGQTLASCGADKTLQVKAETGEKLLETAHEDEVLCAAFSTODRFA 673
Db 5 HAKEYOGISFSPDKMLASASDDNTVKLWDITTGKEIKLTGHTNSVGLGSFSPGKMLA 64

Qy 674 TCSVDKVKIWKNSMTGMBLVHVTYDDESEQNCNCHFTNSSHILLATSSDCFLKLMWLNQK 733
Db 6 SASSDTIVKLWDITTGKEIKLTGHTNSVLGTSF--SPGKMLASASDDNTVKLMDTTG 122

Qy 734 ECRNTMFGHTNSVNHCRFSPDDKLASSCAGTGLKWDATSAKERKSINVKQFFNLDP 793
Db 123 KEIKLTGHTNSVGLGSFSPGKMLASASDDNTVKLWDITTGKEIKLT 170

Qy 794 QEDMBTVKCCWSADGARINVAARKTRFLDIHTSGLGLERHTGHSTQYCDISPOH 853
Db 171 -----TGHRSVFGISFSPDGK 187

Qy 854 LAVVALSQYCVELWNTDSRSKVAADCGRHLSMVGHGMFSPDGSSFLTSSDDOTIRWETK- 912
Db 188 MLASAFDNTVKLWDITTGKEIKLTGHTNSVNDISFSPDKMLASASDDNTVKLMDTT 247

Qy 913 -KVCNSAVMVKQEVDFVQFEMEVNLAVDHIRRQLINERTG-QIDYL-T-EAOVSCCC 968
Db 248 GKEIKLTGHTNSVNDISFSPNGKMLASASFDNTVKLWDITTGKEIKLTGHTNSVNDIS 307

Qy 969 LSPHLOYTAIFDENGALTELEVNNRIIFQHKTWTWHIOFTADEKLTJSSSDAERIQ 1028
Db 308 FSPDGKMLASASGDNTVKLWDITTGKEIKLTGHTNSVNDISFSPDGKMLASASGDNTVK 367

Qy 1029 VNNWQLDKCI-FLRGHQETVKDFRLKNSRSL-SNSFDGTWVKNNTITGENKEKDFVCHQG 1086
Db 368 LWDTTGKEIKLTGHTNSVNGISFSPDGKMLASASGDCKTVLWDITTGKEIKLTGHTN 427

Qy 1087 TVLSCDISHDATKFSSTSADTKAFTKMSFDPLLPHLRGHNGCVRCSAFSYDSTLATEGD 1146
Db 428 SVNGISFSPDGKMLASASGDCKTVLWDITTGKEIKLTGHTNSVNGISFSPDGKMLASAS 487

Qy 1147 DNGEIIWN-VSGNELLHCAPLSEGAATHGGWTDLCFSPDGKMLISAG--GYTKWN 1203
Db 488 SDNTVKLWDITTGKEIKLTGHTNSVNGISFSPDGKMLASASDDNTVKLND 539

Qy 1204 VVTGESSOTFYTINGTN-LKTKHVSPPDFK--TYVTVDN-----LGTLYILQ 1245
Db 540 TTGKBEIKTL-TGHTNWVYGISFSPDGKMLASASDDNTVKLWRDFFYLIQ 589

Query Match 10.4%; Score 688; DB 14; Length 1005;
Best Local Similarity 24.6%; Pred. No. 2e-45; Matches 212; Conservative 163; Mismatches 348; Indels 140; Gaps 21;

Qy 407 ETEVEDILQFVNKSLLFCDFRNGSFRYL-HDLQDFLITEKNGSQLDQHKKITQFQ 465
Db 239 BINKDLILEFVQSGCLVVLLENPADRYQLVHDIAAFTRQQBPKL---KQVMABLE 294

Qy 466 RYHQPHTLSPPQEDCMYWWYNFLAYMASAKMKHEKCALMFSLDWIKAKTELVGP AHLHE 525
Db 295 KERKERKLS-----EARLNSFKRALKST--VAAGLGFAGLAAATFQ 334

Qy 526 FVEYRHLDEKDCAVSENFOQELSLNGH----LIGROPPPNIVQL-----GLCEPE 572
Db 335 W-----AVEANVNOISAINNSSEAFLSEKYPDALIAAKGSKLKHTLWAQH 382

Qy 573 TSEVYQAOQKLAOKAOVADNGMLYLEVINKRNITNLNRLVVRPHTDAYHACTSEGORIAS 632
Db 383 RSDIMQTVTQLQAV----YLKEKEKKENRAIETVNTLGHSDWTVSSVASYSPNGYQLAS 437

Qy 633 CGADKTLQVFAETGKELBLIKAHEDEVLCCAFSTDDRFATCSTDCKVVKIWNSTMGTGELY 692
Db 438 ASADTTKIVDVSSEOLLKTLGHDRIIRATSYNSQGQQLVASASDRTKIVDVSSEGKLL 497

Qy 693 HTYDDEHSBQVNCCHTFTNSHLLATGSSDFCLKWLDMNOKECRNTMFEHTNSVNHCRFS 752
Db 498 KTLTGHTSAVSSVATNPNGQ---LASASDDNTVKLWDISSGKLLKTLPGHSSVNVSVAYN 555

Qy 753 PDDKLLASCSADGTKLWDATSAKSBNKSTVQKFQFLNEDQEDNEVIRCCSWSADGAR 812
Db 556 PNGQOLASASNDKTKIWIINDNSKGKLLSQTGHSSSEVN-----SVAYSBNQGQ 602

Qy 813 IMVA--KKNKFLFEDHTSGLGEIHTGHSHSTQYCDFSQNHLAVVVALSQYCVELWNTDS 871
Db 603 LASASPDNTVKIWD-SSGRULKLTGHSANVLAASASDRTKIVDVSSE 661

Qy 872 RSKVADCRGHLISWVGYMFSPDGSSFLTSSDDQTRLWETKVKVCHNSAVMLKQEVDTVVFQ 931
Db 662 GKPLKSLAGHSNNVVPSSVAVSPNGQOLASASDSDTKIVD-----700

Qy 932 ENEVAVLAVDHIRRLQLINGRTQDYLTLE-AQVSCCUSPHLOVYTAIFDENGALTE 989
Db 701 -----ISNGK---PLESMTDHSDRNISVUTVSPNGQHLASPSYDRTKIVN 742

Qy 990 LVNNRIFQSFRQHKKTVWHIQFTADEKTLJSSDPAEIQVNWOLDKCI-FLRGHQETVK 1048
Db 743 VSSGTLKLTGHSSEVNSTVSPQGQQLASASWRTKIVDVSNSKPLTKLIGISSVNN 802

Qy 1049 DFLLKNN-SPILLSWSPDTGTVKWNJLITGNKEKDFVQHGTLSCDFISDATHKFSTSADK 1107
Db 803 SVAYSBNQGQOLASASFDNTKIVDVSSEKLLKTLGHSDAVSSVAVSPNGQOLASASLDN 862

Qy 1108 TAKTWSFDLILPLHBRGNGCVRSAFSYDSTLATEGGEITRINWVNGELLHLHCAPI 1167
Db 863 TIKINDVSSAKLLKTLGHSDAVSSVAVSPNGQOLASASDNTKIVDVSSEGKLL-----917

Qy 1168 LSEEGBAATHGCGWYDLCFSPDGKMLISAG-GYIKMWVNTGESSQ-----TF 1213
Db 918 ---KSLSGHESNAVYSAYSVPNQGQOLASASADNTKIVDVSSEKLLKTLGHSDWVMRVTV 974

Qy 1214 YTNGTMKXKTHVSPDFKTVVD 1236

RESULT 13
US-10-369-493-20242
; Sequence 20242, Application US/10369493
; GENERAL INFORMATION:
; Publication No. US20030233675A1
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianteng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052) B

Db	975	NPQQLASASV--KTIWLD	9 94
Db	975	RESULT 14 Sequence 1-93-19053 ; Sequence 19053, Application US/10369493 ; GENERAL INFORMATION: ; PUBLICATOR: US20030233675A1 ; APPLICANT: Cao, Yongwei ; APPLICANT: Hinkle, Gregory J. ; APPLICANT: Slater, Steven C. ; APPLICANT: Goldham, Barry S. ; APPLICANT: Chen, Xianfeng	
Db	975	TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10152052 B CURRENT APPLICATION NUMBER: US/10/369,493 PRIOR APPLICATION NUMBER: US 60/360,039 PRIOR FILING DATE: 2002-02-21 NUMBER OF SEQ ID NOS: 47374 SEQ ID NO 19053 LENGTH: 1140 TYPE: PRT ORGANISM: Anabaena FCC7120 US-10-369-493-19053	
Query	126	FVTRKKLVNAIOQKLSKUKKGKPGWWTTHGMAGCKSV----LAAEAVRDHSLLLEGCPFG 180 21 FYGRLITLTT--QQLIADLANK-SFMAYVGSSGSVSVQAGLIAQRGRGQL----PG 71	
Db	181	GHWWSVGKDKDSGLMLQNLCTRDQDFSFORSRPLN---IEAKDRURILMURKHP 236 72 SOEWWNMSFRPGEYPLVSLSHCLVDSGETEKAYQOMQLEGMLYQGAQGFVWHLHREP 131	
Query	237	RSLLIIDDDWSWLRKAQDSQCOLLT----TRDK----SVTDSVMGPKVYPVES 284 132 MVLVLDQFPEELTAAEDDRFLDTVLGALESPDKPLKLTVLRAFDIAFACLEPTLA 191	
Db	285	SLGKKGK----EILSLFVN-MKCADL--PQEAHSLIKECKGSPLVLSLIGALL 331 192 KLLQSSILLUPCITQEEYRRIIIHPAKVLTVDPELVELVQLOELINSPGDLPLLEFVL 251	
Query	332	RDFPNRWEY-----YKLQONQKQFKRKSYYDTEALD_EAMS----IS 371 252 EQL---WEIRDKGVITLQAYQYLQGKKG---ALEKQAOQYDITLSEQAQCTRWMFLS 304	
Db	372	VEMLRED-----IKTDYTDLSLQDVKVPTKVCLYLWDMETEE----410	
Db	305	LTDQSEGDTTRRVLKSELIVKY----PVAVLERTVQVLTVAEVKLYNEFGRGRKRG 362 411 -----VEDIQ----EFUNKSLFCDRNGSKRYYLHDLOQVDFTERNCSQLDLH 457	
Db	363	AGGRGGENILLTTPSVTIEVAHEVII---RYWSTLRWV----EENRSRLR-S-H 409	
Query	458	KKITOFQRYHQPHLSPD-----QEDCMYN-YNFL--AYHMASAKM 496 410 :-----RQ-IESSAALWQNNQQDPFLQGQVRLAABEYIYNTBLSDVQHFIIEALHERRKQ 468	
Db	497	HKELCALMFSLDWIKATEL---VGAFAHLEFVEYRHLDEDC-AVSENF---QEP 547 469 NQEQRSLRQBQRAYVISTLGLTAFAVAYQOTONAQLKEOQALNSLNELLSKQL 528	
Query	548	LSLNGHLLGRQFPPNIVQGLL--CEPHTSEVYQOKLAQQEYDNLNWLKNIT 604 529 EALMNTSVQACKEVONI-SLGPIDPDITQTATIQLQQAVENTQER---NLUHNWV---VT 580	
Db	605	NLSRLVVRPHTDAYTHAFSESDQRJASCGADKTLQVKAETGEKLIKAEDEVUCCA 664	
Db	581	SVS-----YSPDGEVETASGSYDNTLHLWRD-GKLITLTGINDGYNSVS 624	
Query	665	FSTDIDRFIATCSVDKVKIWNNSMTGELVHYDEHSEQNCCHFTNSSHHLIATGSSDCF 724 625 FSPDGEILASASADSTIKW-ORNGQJITLKGHDQGVKSFSPAGE--IIASGSDHT 681	
Query	725	LKLWDINQECRNTMFGHTNSYNHCFSPPDQKLASSADGTLKWLWATSAERKSINVK 784 682 INLWSRAGK-LLLSLNGHSQGNTSIRESPGEGTDAASADDGTIRLW--SLDGRPLUTI- 736	
Db	785	QFFNLAEDPOEDMEVYKCCSYASDARAWYA-AKNIKLFDIHTSGLGEIHTGHSHSTI 843 737 -----PSHTKX--AVTESPDQCVTISAGADNTVQLWS--RNGLTLLTLEGNEAV 784	
Query	844	QCDCDFSPONHLLAVVLSQCYCVELWNTDSRKSVADCRGHLMSWVHGMSFPDGSSELTSD 903 785 WQVISPDRGLIATASADKTFLWSRD-NILGTFAGHNEVNSLSPDGNILASGSDD 843	
Db	904	QTIRIWMETKVKVCKNSAATMLKQEVDFVFOENE---VMVLAVIDHTRRQLINGRTQDYLTLT 960 844 NTVRLLWNTVRLPLPKTGYHKGSVSYTRFSNDGKKTISLSTSTMKTSLSLGLQTLSSP 903	
Query	961	BAQVSCCCLUSPHQYIAGDENGATEBILLYNRR--IPOSREFOKHVTWHLQFTADEKT 1017 Db	
Db	904	LPDVTSISSTDPKVIALASPHTLY---NRCQGULLRSUPGHNWITSLSPSPNKOI 959 1018 LISSSDDABQW--NWLQDCFLYRQHETKDFVPLKLNRSR-LLSNSPDGTUVKVNINIT 1074 960 LASGADTKLWNSVNRLLT-LIGHNSWVTDLKFSADGKNTVSASADTKTWS-LD 1016	
Query	1075	GNKBRDFVCHQGTVLSCDISHDATKESSTDADTAKINGFDULPLPHELGNGCVRCSA 1134 1017 GRLITLQOHSASWVSNLSPDGQTLASTSQDENTKLWNLNGEL-ITYLRLGHSDVYTNL 1075	
Db	1135	FSVDSLTLATGDDNGEIRWVNSGFLHLHCAPILESEGATHGGWVTDLCFSPDGRMLIS 1194 Db	
Db	1076	FSPDGKTAASADSDGTLKLNWNPNTLW---TFQG--HRGGVSVSFSPDGKTLAS 1127 Query	
Query	1195	AGY--IKWANW 1204 Db	
Db	1128	-GGHTTVKWNL 1139	
RESULT	15	US-10-369-493-19046	
		; Sequence 19046, Application US/10369493	
		; General Information:	
		; Sequence 19046, Application No. US20030233675A1	
		; Applicant: Cao, Yongwei	
		; Applicant: Hinkle, Gregory J.	
		; Applicant: Slater, Steven C.	
		; Applicant: Goldham, Barry S.	
		; Applicant: Chen, Xianfeng	
		; Title of Invention: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF PLANTS WITH IMPROVED PROPERTIES	
		; Title of Invention: PLANTS WITH IMPROVED PROPERTIES	
		; File Reference: 38-10152052 B	
		; Current Application Number: US/10/369,493	
		; Prior Application Number: US 60/360,039	
		; Prior Filing Date: 2002-02-21	
		; Number of Seq ID Nos: 47374	
		; Seq ID No 19046	
		; Length: 1136;	
		; Best Local Similarity 23.2%; Pred. No. 4.7e-44;	
		; Matches 281; Conservative 196; Mismatches 490; Gaps 41;	
Query	95	SSSGKDSVSGTISYYVRTVLCEGYVQRPVVFTRKLVNAIQQKLSKLKGEPGVNTIHG 154	

46 ASGSGKSS-----VVQAGLIPQ---LRQKRHINPSEQWGIKTR--PGVNPLEA 89
 Qy 15 MAGGGKSVLAAZAVRDHSISLLEGF----PGYVHWVSYVKQDKSGLM---KLNQNLCTRL 206
 Db 90 LAR-----KLGEGETHLIIEGLMHQSGTEGFYIWLRSIUPQGTIVLVIDQFEEBLTLPAPT 144
 Qy 207 DODDEFSORPLNTEAEDRLMURKPRSLLIDDDWVSDWVKAIFDSQCQILLTRD 266
 Qy 145 DR EFLFELLGAVQYAGDRFKLII-----TIR-----172
 Db 173 -----DFAPCLPVPALEALQAVSLV--PPKLSDDYRRVTLPAQQVGLQVEA 221
 Qy 267 KSVTDSYNGPKYVVPVSESLGKEKGFLTSLFVNMKKAIDLPEQAHSITIKECK--GSPLVV 324
 Db 178 -----DFAPCLPVPALEALQAVSLV--PPKLSDDYRRVTLPAQQVGLQVEA 221
 Search completed: January 27, 2005, 18:53:21
 Job time : 178 secs

325 SLIGALAR-----DPNRWHEYYLQOLQNQFKRIRKSSSYD-----360
 Db 222 ELEYVLLERLNQSVGDLPLLEFVLEQWQORTAGKLTLTOSYEQEGGIGGALERSCQGV 280
 Qy 361 YEALDBAMS-----ISVEMREDIKD-----SILQKDVKVPTPKVL 401
 Db 281 YESLPPQLQECAKWIPLSLTQLGEGTEDTRRIYKSDLIVKYPAGLVEQTINVLTMAKL 340
 Qy 402 ILWDMETEVEDILQEPVNKSLLFCDRNGKSFRYLHDLQYDFLTENKNCSQLDLHKKKII 461
 Qy 403 RWMILEENRDRLRKQRQINHACQIWIQOSGKQADF---LOGARLAEADIVIYWTDELGAD 441
 Db 341 VVNEAB-----IEAQGKSFSPTPNLSTPFTVTEVAHILRHMSTL 384
 Qy 462 TOFORVHQPHTLSPDQ--EDCMWY----NFLATHMASAKMHRKELCMLSDFWIKAK 513
 Qy 463 RWL-----GHLIGRQPFPNTIVQGLCEPBTSEVYQQAKLQAKOEVNDGMYLEWINKNIT 604
 Db 502 ALNSSSOANLNSHQLAALI-----ASLKAQVNHVIAPNNLKLATVT 546
 Qy 605 NLSRLV-----VRPHTDAYHAFCSEDGORIASCGADKTLOVKFAEKESKLEIAKH 656
 Db 547 TLQQALFEMOBRNRLQEGKDGVISISIISRDGTIASCLDTKLMWSRD-GRLFRFLNIGH 605
 Qy 657 EDBVLCCAFTSTDRLATCSYDRKVKIWNSHTGELVTHDHSHEQVNCCHFTNNSHHLLL 716
 Db 606 EDAVYSVSFSPPGQTASGGSDKTIKLWQTSGTLKLXITGEQTYNNVYFSPDGKN-L 663
 Qy 717 ATGSSDCFLKWLNLQKCECRNTMFGHTNSYNHCRFSPDCKLULASCADGTLKLWDATSAN 776
 Db 664 ASASSDHISKWLWDTTSQQLMLTGHSAVTVRFSPDGQTIAAGBTDKWLWHRQDGK 723
 Qy 777 ERKSINYKQFFNLEDQEDMEVIVKCCSWASDGAIRMAAKNKFLFIDHTSGLGEIH 836
 Db 724 LLKTLNCHQDWYN-----SLSFSPDGKTLASASADKTIKLWRLADGKLVKTL 770
 Qy 837 TGHHSPTIQYCDPSQNHIAVVALSOQVFLWNTDSSVKAQDRGHSIWSWCHGVMFSPDGS 896
 Db 771 KCHANDSUWDNFNSSDGKAIASASRDTKLMRNG-JELFTGHTGGVTAVNFELEDSNI 829
 Qy 897 PLTSSDDQOTIRLW-----TKKVKCKNSAVALMKOEYDVVFQENEVNYLAUDHIRRLQLIN 950
 Db 830 IASASLNTDNTLWRQRLPLSPLVLAGNSGYA-----VSFHHDGSIATAGADGNTQLWH 884
 Qy 951 GRTGQIDYLTEAQVSCCCS--PHLQYIAFGDENGIAILLELNVNRRIFQSRFQHCKTWH 1008
 Db 885 SQDGSLLKTLPGKNAKYGISPTPQGDLLIASANADKTIKLWRLDGRALKTLIGHDNEVNR 944
 Qy 1009 IQFTADEBKTLSSDDAEIQLQWNWQLDKCF---LRGHQETVKDPRLLKNSRLL-SWSFD 1064
 Db 945 VNFSPDGKTLASASRDTKLMWNSDGK--FKKTLKGHTDEUFWVTFSPDGKIIASASAD 1002
 Qy 1065 GTVKWVNITGENKEKDFVCHQGTVLSCDISHDATKPSSTSADKTAKIW-SFDLILPLHNL 1123
 Db 1003 KTIRLWDSFGNLKSLPAHNDLVSFNFDGSMLASTSDKTVLWRSHDGHL-LHTRP 1061



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OM protein - protein search, using sw model

Run on: January 27, 2005, 18:32:45 ; Search time 27 Seconds
 (without alignments)
 3065.365 Million cell updates/sec

Title: US-10-646-396-2

Perfect score: 6619

Sequence: 1 MDAKARNCLLQHREALKEKDII.....PXTYYTVVDNLGLYILQTLTE 1248

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*
 1: /cgn2_6/poddata/1/iaa/5A_COMB.pep:
 2: /cgn2_6/poddata/1/iaa/5B_COMB.pep:
 3: /cgn2_6/poddata/1/iaa/6A_COMB.pep:
 4: /cgn2_6/poddata/1/iaa/6B_COMB.pep:
 5: /cgn2_6/poddata/1/iaa/PECTUS_COMB.pep:
 6: /cgn2_6/poddata/1/iaa/backfives1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6352.5	96.0	1205	3 US-09-092-008-16	Sequence 16, Appl
2	6352.5	96.0	1205	3 US-09-435-115-16	Sequence 16, Appl
3	6282	94.9	1194	3 US-09-192-508-2	Sequence 2, Appl
4	6282	94.9	1194	3 US-09-435-115-2	Sequence 2, Appl
5	6282	94.9	1194	3 US-09-069-023-26	Sequence 26, Appl
6	6282	94.9	1194	4 US-09-198-310-2	Sequence 2, Appl
7	6282	94.9	1194	4 US-09-338-092-825	Sequence 825, App
8	408	6.2	2627	2 US-08-751-189-3	Sequence 3, Appl
9	408	6.2	2627	3 US-09-160-336-3	Sequence 3, Appl
10	408	6.2	2627	3 US-09-184-445-3	Sequence 3, Appl
11	399.5	6.0	2629	2 US-08-751-189-4	Sequence 4, Appl
12	399.5	6.0	2629	2 US-09-160-336-4	Sequence 4, Appl
13	399.5	6.0	2629	3 US-09-184-445-4	Sequence 4, Appl
14	322	4.9	251	4 US-09-291-170A-13	Sequence 13, Appl
15	322	4.9	251	4 US-09-724-592-13	Sequence 13, Appl
16	322	4.9	251	4 US-09-724-592-13	Sequence 13, Appl
17	316	4.8	514	1 US-08-190-802A-66	Sequence 66, Appl
18	316	4.8	514	3 US-08-777-346-66	Sequence 66, Appl
19	316	4.8	514	3 US-08-473-089-66	Sequence 66, Appl
20	316	4.8	514	4 US-08-487-072A-66	Sequence 66, Appl
21	312	4.7	409	1 US-08-190-802A-51	Sequence 51, Appl
22	312	4.7	409	3 US-08-477-346-51	Sequence 51, Appl
23	312	4.7	409	3 US-08-473-089-51	Sequence 51, Appl
24	312	4.7	409	4 US-08-487-072A-51	Sequence 51, Appl
25	311.5	4.7	409	2 US-08-283-917-3	Sequence 3, Appl
26	311.5	4.7	409	2 US-08-961-116-3	Sequence 3, Appl
27	311.5	4.7	409	4 US-09-538-092-1119	Sequence 1119, Ap

ALIGNMENTS

RESULT 1
 US-092-508-16
 Sequence 16, Application US/09092508
 Patent No. 6291613

GENERAL INFORMATION:

APPLICANT: Henzel, William J.,
 TITLE OF INVENTION: APPF-1, AN ACTIVATOR OF C ASPASE-3
 NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
 STREET: 3100 No. 6291643west Center, 90 South Seventh St
 CITY: Minneapolis
 STATE: MN
 COUNTRY: USA
 ZIP: 55402

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/092.508
 FILING DATE: 05-JUN-1998
 CLASSIFICATION: 05:ATTORNEY/AGENT INFORMATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 60/048,807
 FILING DATE: 05-JUN-1997
 APPLICATION NUMBER: 60/055,258
 FILING DATE: 07-AUG-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Kettelberger, Ph.D., Denise M
 REGISTRATION NUMBER: 33,944
 REFERENCE/DOCKET NUMBER: 11669.GUSU1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 612-332-5300
 TELEFAX: 612-332-9081
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1205 amino acids
 TYPE: amino acid
 SPANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FRAGMENT TYPE: internal
 US-09-092-508-16

Query Match Score 6352.5 ; DB 3 ; Length 1205;
 Best Local Similarity 96.6% ; Pred. No. 0 ; Mismatches 0 ; Indels 43 ; Gaps 1;

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Qy	1201	WWVVVTGESSCFYTINGTNLKIHIVSPDFKTVTVDNGLYIQLTE	1248
Db	1158	WWVVVTGESSCFYTINGTNLKIHIVSPDFKTVTVDNGLYIQLTE	1205
Qy	181	GTHWWSVGKDKSGIILMKLQNLQNLQNLQNLQNLQNLQNLQNLTRLDQESFSQRLNTEAKDRILMRKHRSLL	240
Db	181	GTHWWSVGKDKSGIILMKLQNLQNLQNLQNLQNLQNLQNLQNLTRLDQESFSQRLNTEAKDRILMRKHRSLL	240
Qy	241	ILDDYWDSSWLKAQFSDQCOLLTTRDKSVTVSMPKTYVPVSSLGKEKGEBLISLFVN	300
Db	241	ILDDYWDSSWLKAQFSDQCOLLTTRDKSVTVSMPKTYVPVSSLGKEKGEBLISLFVN	300
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Qy	361	YEALDEAMSISVEMREDIKDYXTDISLOQDVVKPTKULCLAMDMEETEVFDILOBFVN	420
Db	361	YEALDEAMSISVEMREDIKDYXTDISLOQDVVKPTKULCLAMDMEETEVFDILOBFVN	420
Qy	421	KSLLPFCDRNGKSFRYTLHDLQVDFLTEKNCSQDLHKKITTOFORYTHOPHTLSPQEDC	480
Db	421	KSLLPFCDRNGKSFRYTLHDLQVDFLTEKNCSQDLHKKITTOFORYTHOPHTLSPQEDC	480
Qy	481	MYWNFLAYIMASAKMHCALMSLDWIAKTELVGPAHLTHEFYRHLDBKDCAV	540
Db	481	MYWNFLAYIMASAKMHCALMSLDWIAKTELVGPAHLTHEFYRHLDBKDCAV	540
Qy	541	SENFOEFSLNLGHGROPNVQVLGCEPTESEVQQLQKQEVTDNGLYLEWINK	600
Db	541	SENFOEFSLNLGHGROPNVQVLGCEPTESEVQQLQKQEVTDNGLYLEWINK	600
Qy	601	KNTNLSRLYRPHDATHYACFSESDGORIASCGADKTKLQVYKABEGKFLRIKAHEDRV	660
Db	601	KNTNLSRLYRPHDATHYACFSESDGORIASCGADKTKLQVYKABEGKFLRIKAHEDRV	660
Qy	661	LCCAFSTDDETRATCSVDKVKLWNSTMGEVHTYDHSEQNCFCFTNSSHLLATGS	720
Db	661	LCCAFSTDDETRATCSVDKVKLWNSTMGEVHTYDHSEQNCFCFTNSSHLLATGS	720
Qy	721	SDGFLKWLWDNQKECRNTMFGHTNSVNHCRSPDDKLASCSDGTLKWDTSANERKS	780
Db	721	SDGFLKWLWDNQKECRNTMFGHTNSVNHCRSPDDKLASCSDGTLKWDTSANERKS	780
Qy	781	INVKQFLINLDQDMENTVKCCSWASDGRIMYAAKWKPLDHTSGLGEHTGHH	840
Db	781	INVKQFLINLDQDMENTVKCCSWASDGRIMYAAKWKPLDHTSGLGEHTGHH	840
Qy	841	STIQYCDFSPONHLAVVALSOYCVELNNTDSRSKYADCRGHLSTWVHGWMFSPDGSSLTS	822
Db	822	STIQYCDFSPONHLAVVALSOYCVELNNTDSRSKYADCRGHLSTWVHGWMFSPDGSSLTS	857-
Qy	901	SDDQTIRLWETKVKCKNSAVMLKOEVDVVFQNEVMYLAQHTRQLQINGTGQDYL	960
Db	858	SDDQTIRLWETKVKCKNSAVMLKOEVDVVFQNEVMYLAQHTRQLQINGTGQDYL	917
Qy	961	EAQVSCCLSPHQTAFGDENGAIELDELNNRIFQSRQHQCTWVHQPADEXTLIS	1020
Db	918	EAQVSCCLSPHQTAFGDENGAIELDELNNRIFQSRQHQCTWVHQPADEXTLIS	977
Qy	1021	SSDAEIQVWNWQLDKCIFRGHOETVKDRLKNSRLIWSFDTVKWNITGNKEKD	1080
Db	978	SSDAEIQVWNWQLDKCIFRGHOETVKDRLKNSRLIWSFDTVKWNITGNKEKD	1037
Qy	121	QRPVVFTRKLVLYNAIQQKLSKLGKBPGWTVTIRGMAGCGKSVLAFAVRDHSLEEGCFFG	180

Db	121	QRPVVVFTRKLVNAIQQKLSQLKGPGWVTHGMAGCKSVLAABRDSSLBSCFPNG	180		1158	WWVVVTGESSOTPYTNTNLKIHVSPDFKTYTVTVDNLGILYILOTLE	1205
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Qy	241	ILDDWDWSWVKAFAFSQCLLTTDKSYTDSVMGPKVYVPESSIGKEGLEILSLFVN	300	; Patent No. 6291643			
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Qy	301	MKKADLPQASISIKECKGSPLVSLIGALDRDPNRYEYTLKOLONKQFKRISSYD	360	; APPLICANT: Hanel, William J.			
Db	301	MKKADLPQASISIKECKGSPLVSLIGALDRDPNRYEYTLKOLONKQFKRISSYD	360	; TITLE OF INVENTION: APF-1, AN ACTIVATOR OF C ASPASE-3			
Qy	361	YEALDEAMSISEYMLREDIDQYTDISLQDKVYPTKVLCTLWMDNETEYDLOQEFVN	420	; NUMBER OF SEQUENCES: 16			
Db	361	YEALDEAMSISEYMLREDIDQYTDISLQDKVYPTKVLCTLWMDNETEYDLOQEFVN	420	; CORRESPONDENCE ADDRESS:			
Qy	421	KSLLFCDRNGKSFRYTLHLDQDFLTENKNSQDQHKLITQFORYHQPHTLSPQBD	480	; ADDRESS: Merchant, Gould, Smith, Edell, Walter & Schmidt			
Db	421	KSLLFCDRNGKSFRYTLHLDQDFLTENKNSQDQHKLITQFORYHQPHTLSPQBD	480	; STREET: 3100 No. 6291643west Center, 90 South Seventh St			
Qy	481	MYWNFLAYHMASAKWKKELCALMPSLWIKAKTELYGPAAHLHETVEYLHILDEKDCAV	540	; CITY: Minneapolis			
Db	481	MYWNFLAYHMASAKWKKELCALMPSLWIKAKTELYGPAAHLHETVEYLHILDEKDCAV	540	; STATE: MN			
Qy	541	SENQETLSLNGHLLGRQPFNIVOLGLCPETSEYQOAKLQAOEVQDNMLYLEWINK	600	; COUNTRY: USA			
Db	541	SENQETLSLNGHLLGRQPFNIVOLGLCPETSEYQOAKLQAOEVQDNMLYLEWINK	600	; ZIP: 55402			
Qy	601	KNITNLSSRLVYVRPHTDAVYHACFSEDQRIASCADKTQVKAFETGEKLLBKRAHEDEV	660	COMPUTER READABLE FORM:			
Db	601	KNITNLSSRLVYVRPHTDAVYHACFSEDQRIASCADKTQVKAFETGEKLLBKRAHEDEV	660	COMPUTER: IBM Compatible			
Qy	661	LCCAFSTDIDRFATCSYDCKYKINNSMTGELVHTDEHSSEQNCCHFTNSHILLATGS	720	OPERATING SYSTEM: DOS			
Db	661	LCCAFSTDIDRFATCSYDCKYKINNSMTGELVHTDEHSSEQNCCHFTNSHILLATGS	720	POST SEQ FOR Windows Version 2.0			
Qy	721	SDCFKLWDLNQKECRNTMFGHTNSTYCRSPDDKLASSADGTLKLMDATSANERKS	780	CURRENT APPLICATION DATA:			
Db	721	SDCFKLWDLNQKECRNTMFGHTNSTYCRSPDDKLASSADGTLKLMDATSANERKS	780	APPLICATION NUMBER: US/09/092,508			
Qy	781	INVKOPPLNLDEQDMEVYTKCCSMASD GARIMYAKNKLFDFDHTSGLGBHTGH	840	FILING DATE: 05-JUN-1998			
Db	781	INVKOPPLNLDEQDMEVYTKCCSMASD GARIMYAKNKLFDFDHTSGLGBHTGH	840	CLASSIFICATION:			
Qy	841	STIQYCDFSPONHLAVALSQYCVELWNTDSRSKVAQDGrimyaknclf-----	900	PRIOR APPLICATION DATA:			
Db	823	-----LWNTDSRSKVAQDGrimyaknclf-----	857	APPLICATION NUMBER: 60/048, 807			
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Db	958	SDDQTIRLWETKVKCNSAVALKOETVDFNEVNLAVDHIRRIQLINGRTQDYL	917	FILE NUMBER: 60/055, 258			
Qy	961	EAQVSCCCLSPHQYAFGDENGATELLVNNRIFOSRFHKKTVWHIOFTADEKTLIS	1020	ATTORNEY/AGENT INFORMATION:			
Db	918	EAQVSCCCLSPHQYAFGDENGATELLVNNRIFOSRFHKKTVWHIOFTADEKTLIS	977	NAME: Kettlerberger, Ph.D., Denise M			
Qy	1021	SDDDAEQWVNNWOLDKCIPLRQHETYKDFRLLNSRLSNSFDGTYKVNNTITGNKEKD	1080	REGISTRATION NUMBER: 33,924			
Db	978	SDDDAEQWVNNWOLDKCIPLRQHETYKDFRLLNSRLSNSFDGTYKVNNTITGNKEKD	1037	REFERENCE/DOCKET NUMBER: 11669 . GUSU1			
Qy	1081	FVCHQGTVLSCDISHATKFSTSADTKTAKIWSFDLLPLBLRGENGTYRCSAFSVDT	1140	TELECOMMUNICATION INFORMATION:			
Db	1038	FVCHQGTVLSCDISHATKFSTSADTKTAKIWSFDLLPLBLRGENGTYRCSAFSVDT	1097	TELEPHONE: 612-332-5300			
Qy	1141	LLATGDDNGBTRIMVNSGELHLHCAPLSSEGAAATHGGWTDLCFSPDGMNLISAGGYK	1200	TELEFAX: 612-332-9081			
Db	1098	LJATGDDNGBTRIMVNSGELHLHCAPLSSEGAAATHGGWTDLCFSPDGMNLISAGGYK	1157	A.			
Qy	1201	WWVVVTGESSOTPYTNTNLKIHVSPDFKTYTVTVDNLGILYILOTLE	1248	INFORMATION FOR SEQ ID NO: 2:			
Db	230	WWVVVTGESSOTPYTNTNLKIHVSPDFKTYTVTVDNLGILYILOTLE	1248	SEQUENCE CHARACTERISTICS:			
Qy	241	ILDDWDWSWVKAFAQSQCQIILTTRDKSYTDSVMGPKYVPESSIGKEKGLEILSLFVN	300	LENGTH: 1194 amino acids			
Db	230	ILDDWDWSWVKAFAQSQCQIILTTRDKSYTDSVMGPKYVPESSIGKEKGLEILSLFVN	289	TYPE: amino acid			

NUMBER OF SEQUENCES: 16
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Merchant, Gould, Smith, Edell, Walter & Schmidt
 STREET: 3100 No. 6346607west Center, 90 South Seventh St.
 CITY: Minneapolis
 STATE: MN
 COUNTRY: USA
 ZIP: 55402
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/435,115
 FILING DATE: 07 AUG 1997
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 09/092,508
 FILING DATE: 07 AUG 1997
 APPLICATION NUMBER: 60/055,258
 FILING DATE: 07 AUG 1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Kettelberger, Ph.D.
 DENISE M
 REGISTRATION NUMBER: 33,924
 REFERENCE/DOCKET NUMBER: 11,669,6USU1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 612-332-5300
 TELEX: 612-332-9081
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1194 amino acids
 STRAND/DNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FRAGMENT TYPE: internal
 US-09-435-115-2

Query 301 MKKADLPQQASIKECKGSPFLVLSIGALLADFPRKWEYLKQLOKQFKRKRSYYD 360
 Db 290 MKKADLPQQASIKECKGSPFLVLSIGALLADFPRKWEYLKQLOKQFKRKRSYYD 349
 Query 361 YEALDEAMISIVEMRLEDIKYTDPLSILQKDYKUPTKULCILIDMPEBEVDILOQFVN 420
 Db 350 YEALDEAMISIVEMRLEDIKYTDPLSILQKDYKUPTKULCILIDMPEBEVDILOQFVN 409
 Db 421 KSLIFCDRNGKSFRYFLHDLOQDFLTKNSCQLQDLHKKTQFORHOPHTLSPQEDC 480
 Db 410 KSLIFCDRNGKSFRYFLHDLOQDFLTERNSCQLQDLHKKTQFORHOPHTLSPQEDC 469
 Query 481 MYYNFLAYHNMSAKNHKECALMFSLWIKARTELVGPAHLINFEVYRHTLDEKDCAV 540
 Db 470 MYYNFLAYHNMSAKNHKECALMFSLWIKARTELVGPAHLINFEVYRHTLDEKDCAV 529
 Query 541 SENFOEFLSLNCHLGRQPFPNTVQLGLCEPTESEYQQLQAKQEVDNGMLYLEWINK 600
 Db 530 SENFOEFLSLNCHLGRQPFPNTVQLGLCEPTESEYQQLQAKQEVDNGMLYLEWINK 589
 Query 601 KNNTNLISLURPHDTAIDYHACSEBDGORIASCGAANTLQVEKETGEKLIEKAHDEV 660
 Db 590 KNNTNLISLURPHDTAIDYHACSEBDGORIASGADKTLOVKATGEKLIEKAHDEV 649
 Query 661 LCCAFSTDDRFATCSVDKVKVTKWNMSMGEVLHTYDEHSRQVNCHFTINSHHLLATGS 720
 Db 650 LCCAFSTDDRFATCSVDKVKVTKWNMSMGEVLHTYDEHSRQVNCHFTINSHHLLATGS 709
 Query 721 SDCFLKWLWDLNOKECRNTMFGHTNSVNHCRFSPDDKLLASADGTLKWDATSAERKS 780
 Db 710 SDCFLKWLWDLNOKECRNTMFGHTNSVNHCRFSPDDKLLASADGTLKWDATSAERKS 769
 Query 781 INVQPFELLDPQEDMEVYKCCSWASDGAIRIMVAKKNPKLFDIHTSGLGEIHTGH 840
 Db 770 INTQFFPLNLLDPQEDMEVYKCCSWASDGAIRIMVAKKNPKLFDIHTSGLGEIHTGH 811
 Query 841 STIQCYCDFSPPONLHAVALVALSOYCVELWNNTDSRKVADCRGHLSKVHGCMFSSPDGSSPLTS 900
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 Db 812 -----
 Query 901 SDDQTIRLWETKVKVCKNSAVMLKOEVDVYFVQNEVNVLAHDHTRRLQINGTQDYL 960
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 Query 961 EAQYSCCCSPLHQTAFGENGIAEIELVNNRIFQSFRQHKCTVWHIQFTADEKTLIS 1020
 Db 907 EAQYSCCCSPLHQTAFGENGIAEIELVNNRIFQSFRQHKCTVWHIQFTADEKTLIS 966
 Query 1021 SSDDAEQVWNWQLDKCIPIRQHETQKDFPLKXSPRLISWSPGTVKWNITGNKEKD 1080
 Db 967 SSDDAEQVWNWQLDKCIPIRQHETQKDFPLKXSPRLISWSPGTVKWNITGNKEKD 1026
 Query 1081 FVCHQGTVLSCDISHATKESSTSADKATKWSFDTLPLHELRGHNCGVRCSAFSVDST 1140
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 Query 1141 LLATGDDNGEIRIWVNSGELHLICAPLSEGAATHGGNTDLCFSPGKMLISAGYIK 1200
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 Query 1201 WNNVVTCESOFTFYINGTNLKKHVSDFKTYVTVDNLGILYILOQLE 1248
 Db 1147 WNNVVTCESOFTFYINGTNLKKHVSDFKTYVTVDNLGILYILOQLE 1194

RESULT 4
 US 09-435-115-2
 / Sequence 2 Application US/09435115
 ; Patent No. 6346607
 ; GENERAL INFORMATION:
 ; APPLICANT: Henzel, William J.
 ; TITLE OF INVENTION: APAF-1, AN ACTIVATOR OF C ASPASE-3

361 YEALDEAMISIVEMRLEDIKYTDPLSILQKDYKUPTKULCILIDMPEBEVDILOQFVN 420
 Db 350 YEALDEAMISIVEMRLEDIKYTDPLSILQKDYKUPTKULCILIDMPEBEVDILOQFVN 409
 Query 421 KSLIFCDRNGKSFRYFLHDLOQDFLTERNSCQLQDLHKKTQFORHOPHTLSPQEDC 480

Db 410 KSLPFCRNGSFRYLHLDQVDFTEKNC SOLQDLHKITQTQRYHQPHTLSPDQEDC 469
 Qy 481 MYWNLFLAYNMSAKHKEKLCAIMFSLWIKAKTELVPAHLIHFVEYRHLDEKDCAV 540
 Db 470 MYWNLFLAYNMSAKHKEKLCAIMFSLWIKAKTELVPAHLIHFVEYRHLDEKDCAV 529
 Qy 541 SENFOEPLSLNGLGRQPFNPVQIOLGICEPETSEYQQAQLQAKOEVNDMLYLEWINK 600
 Db 530 SENFOEPLSLNGLGRQPFNPVQIOLGICEPETSEYQQAQLQAKOEVNDMLYLEWINK 589
 Qy 601 KNITNLRLVVRPHTDAYHAFAFSEDCORIASGADKTLQVKAETGEKLISIAHDEV 660
 Db 590 KNITNLRLVVRPHTDAYHAFAFSEDCORIASGADKTLQVKAETGEKLISIAHDEV 649
 Qy 661 LCCAFSTDRFATCSYDKYKUWNNTGELVTHDESBQNCCHFTNSBHLIATGS 720
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 Qy 721 SDCFLKLWDLNQKECERNTMFGHTNSYHCRSPDDKLASCSADGTLKLNDATSANERKS 780
 Db 710 SDCFLKLWDLNQKECERNTMFGHTNSYHCRSPDDKLASCSADGTLKLNDATSANERKS 769
 Qy 781 INVQPFPLNLEDQEDMEVIVKCCSKSADGARIMVAARKNIFLFDIHTGHLGEIHTGHH 840
 Db 770 INVQPFPLNLEDQEDMEVIVKCCSKSADGARIMVAARKNIF----- 811
 Db 841 STIQYCDFSQNHLAVVLSQYCVELWNTDERSKVADRGHLSWHGVMSPDGESFLRS 900
 Db 812 -----LWNNTDSRSKVADRGHLSWHGVMSPDGESFLRS 846
 Qy 901 SDDQTIRLWETPKVKCNSAVALMKOEQTDVVFQENEVNVLAVDHIRRLQLINGRTGQDYLIT 960
 Db 847 SDDQTIRLWETPKVKCNSAVALMKOEQTDVVFQENEVNVLAVDHIRRLQLINGRTGQDYLIT 906
 Qy 961 EAQVSCLCSPHLOYAFGDENGAIELLEVNNRIFQSRFQHKCTVWHIOPTADEKTLIS 1020
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 Qy 1021 SSSDAEIQVNWQLDCKTFLGHQETYKDFLQLNSRSLSMSFGTVKWNNIITGENKEKD 1080
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 Qy 1201 WNNVTGESSOFYTNGTNLKIIHVSPDFKTYVTVDNLGLYILOTLE 1248
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RESULT 5
 US -09-069-023-26
 Sequence No. 6348573
 GENERAL INFORMATION:
 APPLICANT: Koseki, Takeyoshi
 APPLICANT: Nunez, Gabriel
 APPLICANT: Inohara, Naohiro
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
 TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
 FILE REFERENCE: UM-03333
 CURRENT APPLICATION NUMBER: US/09/069, 023A
 CURRENT FILING DATE: 1998-04-27
 SEQ ID NO: 26
 LENGTH: 1194

US -09-069-023-26
 Patent No. 6348573
 APPLICANT: Koseki, Takeyoshi
 APPLICANT: Nunez, Gabriel
 APPLICANT: Inohara, Naohiro
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
 TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
 FILE REFERENCE: UM-03333
 NUMBER OF SEQ ID NOS: 38
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 26
 LENGTH: 1194

; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-069-023-26
 Query Match 94.9%; Score 6282; DB 3; Length 1194;
 Best Local Similarity 95.7%; Pred. No. 0;
 Mismatches 0; Indels 54; Gaps 2;
 Matches 1194;
 1 MDAKAQNCLLQHREALEKDITSYIMDHMISDGFLTISEEKVNRNEPTQQRAAMLIKMI 60
 Qy 1 MDAKAQNCLLQHREALEKDITSYIMDHMISDGFLTISEEKVNRNEPTQQRAAMLIKMI 60
 Db 1 MDAKAQNCLLQHREALEKDITSYIMDHMISDGFLTISEEKVNRNEPTQQRAAMLIKMI 60
 Qy 61 LKKDNDSYVSTYNALLHEGYKDAAUHDGIPPVVSSSGKDSVSGITTSYVRTVLCERGGVP 120
 Db 61 LKKDNDSYVSTYNALLHEGYKDAAUHDGIPPVVSSS-----VTVLCERGGVP 120
 Qy 61 LKKDNDSYVSTYNALLHEGYKDAAUHDGIPPVVSSS-----VTVLCERGGVP 109
 Db 121 QRPVVFVTRKCLVNAIQQKLSKLGEPGMVTTMGAGCGKSVLAFAVDRDHSILLEGCPFG 180
 Db 110 QRPVVFVTRKCLVNAIQQKLSKLGEPGMVTTMGAGCGKSVLAFAVDRDHSILLEGCPFG 169
 Qy 181 GVHWVSGKQDKSGLLMQLNQLCTRQDQDESFSQRQPLNTEBKQRLRILMRKHRSLL 240
 Db 170 GVHWVSGKQDKSGLLMQLNQLCTRQDQDESFSQRQPLNTEBKQRLRILMRKHRSLL 229
 Qy 241 ILDDWDSDWVTKAFPSQCOQILTTRDVKSYTDSVMGPKYVPESSLGKEKLEILSLFVN 300
 Db 230 ILDDWDSDWVTKAFPSQCOQILTTRDVKSYTDSVMGPKYVPESSLGKEKLEILSLFVN 289
 Qy 301 MKKADLPQOAHSIIKECKGSPVYVSLIGALLRDFPNRWEYKYLKOLQNKOPKRKRSYYD 360
 Db 290 MKKADLPQOAHSIIKECKGSPVYVSLIGALLRDFPNRWEYKYLKOLQNKOPKRKRSYYD 349
 Qy 361 YEALDBAMSISVEMMRERIDKDYTTDISILQDKDVKYPTKVLCLWMDNETEEVEDILQEFVN 420
 Db 350 YEALDBAMSISVEMMRERIDKDYTTDISILQDKDVKYPTKVLCLWMDNETEEVEDILQEFVN 409
 Qy 421 KSLIFCDRNGKSFRYTLHDQDFLTKEKNSQOLDLHKLKITOFRYHQPTLSPDQEDC 480
 Db 410 KSLIFCDRNGKSFRYTLHDQDFLTKEKNSQOLDLHKLKITOFRYHQPTLSPDQEDC 469
 Qy 481 MYWNLFLAYMASAKHKEKLCAIMFSLWIKAKTELVPAHLIHFVEYRHLDEKDCAV 540
 Db 470 MYWNLFLAYMASAKHKEKLCAIMFSLWIKAKTELVPAHLIHFVEYRHLDEKDCAV 529
 Qy 541 SENFOEPLSLNGLGRQPPNIVQVLGLCPETSVYQQAKLQAKOEVNDGMLYLEWINK 600
 Db 530 SENFOEPLSLNGLGRQPPNIVQVLGLCPETSVYQQAKLQAKOEVNDGMLYLEWINK 589
 Qy 601 KNITNLRLVVRPHTDAYHACSFSDGORTIASGADKTLYQVKAFTEGEKULEIAHDEV 660
 Db 590 KNITNLRLVVRPHTDAYHACSFSDGORTIASGADKTLYQVKAFTEGEKULEIAHDEV 649
 Qy 661 LCCAFSTDDRFIATCSVDKCKVWNMSMTGELVHVTYDEHSEQVNCCHTFTNSHHLJLATGS 720
 Db 650 LCCAFSTDDRFIATCSVDKCKVWNMSMTGELVHVTYDEHSEQVNCCHTFTNSHHLJLATGS 709
 Qy 721 SDCFLKLWDLNQKECRNTMFGHTNSVNHCRSPDKLALLACSCADTLKMDATSNERKS 780
 Db 710 SDCFLKLWDLNQKECRNTMFGHTNSVNHCRSPDKLALLACSCADTLKMDATSNERKS 769
 Qy 781 INVKQFLNLEDQDMEVTKCCWSADGARIYAAKNIFLPDTHTSGLGEHTGH 840
 Db 770 INVKQFLNLEDQDMEVTKCCWSADGARIYAAKNIFL----- 811
 Db 812 -----LWNTDSRSKVADCRGHLSWHGWMESPDSSEFLTS 846
 Qy 841 STIQYCDFSQNHLAVVLSQYCVELWNTDERSKVADRGHLSWHGVMSPDGESFLTS 900
 Db 847 SDDQTRLWETKVKCNSAVMLQEVDDVYFQENETMVLAUDHIRELQLINGRTGIDYL 960
 Qy 961 EAQVSCCLCSPHLOYAFGDENGAIELLEVNNRIFQSRFQHKCTVWHIQPTADEKTLIS 1020

LENGTH: 1194
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE: misc_feature
 LOCATION: (0)..(0)
 OTHER INFORMATION: Polypeptide Accession Number 014727
 US-09-538-092-825

Query Match Score 6282; DB 4; Length 1194;
 Best Local Similarity 95.9%; Pred. No. 0;
 Matches 1194; Conservative 0; Mismatches 0; Indels 54; Gaps 2;

Qy 1 MDAKARNCNLQHREALKEKDITKTSYIMDHMISDGFLTISEEEVKRNNEPTQQRAAMILKMI 60
 Db 1 MDAKARNCNLQHREALKEKDITKTSYIMDHMISDGFLTISEEEVKRNNEPTQQRAAMILKMI 60

Qy 61 LKKDNDSYVSPNALLHEGYKDLAALHDGIPVWSSSSGRDSVSGITSYRTVLCCEGGYP 120
 Db 61 LKKDNDSYVSPNALLHEGYKDLAALHDGIPVWSSSS-----RTVLCCEGGYP 109

Qy 121 QRPVVFTRKLVNAQQKLSKLKGEPGWVTHMGAGCKGSVLAEEAVRHSLLLEGCPFG 180
 Db 110 QRPVVFTRKLVNAQQKLSKLKGEPGWVTHMGAGCKGSVLAEEAVRHSLLLEGCPFG 169

Qy 181 GVHWYSGVKDKDGSGLMLKMLQNLCTRLDQDESFSQRPLNIEEAKDRRLTMLRKHPRSL 240
 Db 170 GVHWYSGVKDKDGSGLMLKMLQNLCTRLDQDESFSQRPLNIEEAKDRRLTMLRKHPRSL 229

Qy 241 ILLDDWDSTWLKAQDSQQLLTRDKSVDTSVMPKTVPESSLGKGGLEILSFVN 300
 Db 230 ILLDDWDSTWLKAQDSQQLLTRDKSVDTSVMPKTVPESSLGKGGLEILSFVN 289

Qy 301 MKKADLPIEQAHISIKECKGSPLVSLIQLGALLRDPTRWETYLKQLOQNKPKRIRKSSSD 360
 Db 290 MKKADLPIEQAHISIKECKGSPLVSLIQLGALLRDPTRWETYLKQLOQNKPKRIRKSSSD 349

Qy 361 YEALDEAMSIYVEMLRDIDKDYDTSLISLQDKVYPTKVLICLDMETEEVEDLQEFPN 420
 Db 350 YEALDEAMSIYVEMLRDIDKDYDTSLISLQDKVYPTKVLICLDMETEEVEDLQEFPN 409

Qy 421 KSSLFCDRNGSFRYLHQDVFLETKNSQOLDLHKKITOPYHQHHTLSPQEDC 480
 Db 410 KSSLFCDRNGSFRYLHQDVFLETKNSQOLDLHKKITOPYHQHHTLSPQEDC 469

Qy 481 MYWNFLAYHMASAKNHKECALMFLDWIKARTELVGPAHLHFVPHILDKCAV 540
 Db 470 MIWNFLAYHMASAKNHKECALMFLDWIKARTELVGPAHLHFVPHILDKCAV 529

Qy 541 SENPQFLSLNGLJLGRQPFPNIVOLGLCPEBTSEVYQOAKLQAKQEVNGMLYLEWINK 600
 Db 530 SENPQFLSLNGLJLGRQPFPNIVOLGLCPEBTSEVYQOAKLQAKQEVNGMLYLEWINK 589

Qy 601 KNITNLSLRVPRHTDAVHACFSEGDQRTASCADKTLQVKATGEKLEIAKDEV 660
 Db 590 KNITNLSLRVPRHTDAVHACFSEGDQRTASCADKTLQVKATGEKLEIAKDEV 649

Qy 661 LCCAFSTDRIATCSVDKCKVTKWNSMTCGELVHTDEHSQVNCCHFTSHILLATGS 720
 Db 650 LCCAFSTDRIATCSVDKCKVTKWNSMTCGELVHTDEHSQVNCCHFTSHILLATGS 709

Qy 721 SDCFLKLWDIINQKECRNTMFGHTNSVNHCRSPDDKLASCSADGTLKWDATSANERKS 780
 Db 710 SDCFLKLWDIINQKECRNTMFGHTNSVNHCRSPDDKLASCSADGTLKWDATSANERKS 769

Qy 781 INVKOPPLNLEDPODMEVYKCCWSADGARIMYAAKNIKFLDIHTSGLGEHTGH 840
 Db 770 INVKOPPLNLEDPODMEVYKCCWSADGARIMYAAKNIKFL-----811

Qy 841 STIQYCDFSQNHLAVVLSOYCVELWNTDSRSKVADCRGHLSWHGMSPDGSSFLTS 900
 Db 812 -----LWNNTDSRSKVADCRGHLSWHGMSPDGSSFLTS 846

Qy 901 SDDQTIRLWETKVKCKNSAVALKOEVDDVFOENETMVLAVIDHIRLQLINGRTGGOIDYL 960
 Db 847 SDDQTIRLWETKVKCKNSAVALKOEVDDVFOENETMVLAVIDHIRLQLINGRTGGOIDYL 906

Qy 961 EAQVSCCCLSPHQVIAFGDENGATEILEELVNRLFQSREFOHKCKTWHIOFTADEKTLIS 1020
 Db 907 EAQVSCCCLSPHQVIAFGDENGATEILEELVNRLFQSREFOHKCKTWHIOFTADEKTLIS 966

Qy 1021 SSDDBEIQWVNWLQKXCIPLRGHQTVKDRLLQSRLLWSFDGTVKWNITGNKEKD 1080
 Db 967 SSDDBEIQWVNWLQKXCIPLRGHQTVKDRLLQSRLLWSFDGTVKWNITGNKEKD 1026

Qy 1081 FVCHQSTVLSISDADATEFSSTDADTKAISFPLLPHLRLHGNGCYRCSAFSVSDST 1140
 Db 1027 FVCHQSTVLSISDADATEFSSTDADTKAISFPLLPHLRLHGNGCYRCSAFSVSDST 1086

Qy 1141 LLATCDDNGEIRIYVNSNGELHIIQAPLSEGAATHGGWYTDLCPSPDGKMLISAGGYIK 1200
 Db 1087 LLATCDDNGEIRIYVNSNGELHIIQAPLSEGAATHGGWYTDLCPSPDGKMLISAGGYIK 1146

Qy 1201 WNWVVTGESSQTFYTINGTNLKKIHSDFKTYTTVDNLGLYLYLQITLE 1248
 Db 1147 WNWVVTGESSQTFYTINGTNLKKIHSDFKTYTTVDNLGLYLYLQITLE 1194

RESULT 8

US-08-751-189-3

Sequence 3, Application US/08751189

Patent No. 5919656

GENERAL INFORMATION:

APPLICANT: Harrington, Lea A.

TITLE OF INVENTION: No. 5919656el. Genes Encoding Telomerase Protein

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESS: Amgen, Inc.

STREET: 1804 De Havilland Drive

CITY: Thousand Oaks

STATE: California

ZIP: 91320-1789

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/751-189

FILING DATE: 15-NOV-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Oleksi, Nancy A.

REGISTRATION NUMBER: 34,688

REFERENCE/DOCKET NUMBER: A-433

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 267 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-08-751-189-3

Query Match 6.2%: Score 408; DB 2; Length 2627;

Best Local Similarity 21.0%; Pred. No. 4.1e-27;

.. Matches 296; Conservative 170; Mismatches 492; Indels 454; Gaps 58;

Qy 97 SSGKGSVSGTSVYVATVCE-----GGVQRPVYVPTRKLYNAIQQCLSK-- 142

Db 1083 AAQRYVYVGGLEEFGQIVLQDPWMMTQKLYQATFQOLQKPP 1141

Qy 143 -----LKSEPVWVTHGMAGGGSVLAEARVDSHSLLEGCPFGV-- 182

183 -----HWSVQDKSGLMLQNLCTRLDQDEFSQRQLPLNTEAKDLRILMLRKHPR 237
 Qy :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 1195 XLVFFPH-SCGARDPQGLATLRLRLCYLRQOLKECALPTYSLWELQQLPKSAE 1253
 Qy 238 SL-----LILD-----DWDSSWLKAEDSQCQIL-TTRDKSVDTSVMGPKYVV 280
 Db 1254 SLHPGOTQVLTDGADRLLDONGOLISWIKLPRCVHLTSVS---SDAGLG--- 1304
 Qy 281 PVESSLGEKGKLEILSLFVANNKKADLPQAHSIILRECKGSPLVVLIGALLRDPNWRBY 340
 Qy 1305 ---ETLEQSOGAHVLL- -GPLEASARALVRE---ELAL 1336
 Db 341 YLKOLONKOFKR-----IRKSSYDYALDBAMSISVEMIREDIKYTDLSLILQKDVK 394
 Qy 1337 YGRLEBSPFNQMRILLVRESGRPLYRLVTDLHRLFTYEQYSERLRLT---PAT 1391
 Qy 395 VPTKVULCILWDMETEEVEDILOEF----YNKSLIFCDR----- 428
 Db 1392 VPLLQHILSTLEKHGPDVLFQALTALEYTRSLGLTVQHGVLSVWRTLFPKGTKSWEA 1451
 Qy 429 --NGKSPRYY-----LHDLOQDFLTENKSQLDILHKKUITQFORYHQPHTLSP 475
 Db 1452 VAAGNSGDPYPMGPFACLVQSURSLIGEPLPERGARLCLPDGPLRTAARCYGKR--P 1508
 Qy 476 DQEDCMY-----W-----YNFLAYTMASAKMHLCALMFSLDWI 510
 Db 1509 GLEDTAHILIAQLWKTICDADASGTPRSCPPBEAGDLPLHILQSGNRGLISKFLTNHVV 1568
 Qy 511 KAKTELVPAHLIHEVY-----RHILDEKDCAVSENFOEELSNGHHLGROPPNI 563
 Db 1569 AAHLELGLVSRULEAHAYASSVPKEEQKGPEADYAV- -FRTFLRQOASLTSQ-YPRL 1623
 Qy 564 V-QLGUCEPETSEVCOAKLQAK---QEVDNGMLYLEWINK---KNITNLS-BLVVRP 613
 Db 1624 LPQQANOPLDSPLQASLSSRMRWFLQHT-----LWLINKPRTMKNQOSSSLAVSS 1677
 Qy 614 HTDAYTHACFESDGORTIASCGADKTLQVKARTGEKLLEIKAHEDDEVCAFSTDRFTA 673
 Db 1678 SPTAV--AFSTINGQRAAVGTANGTYLIDRTQEBKSVSGCDGISAFLSDDTFL 1734
 Qy 674 TCSVDKVKWNSMTGELVITYDEHSEQVNCCHTFTNSSHILLATGSSDCFLKLWDLNQK 733
 Db 1735 T-----AFGDLIELMDL-OH 1748
 Qy 734 ECRNTMF-GHTNSVNHCFSRSPDDKLLASCADGTLKWD-----ATSANERKSINVQKF 786
 Db 1749 GCRVLQTKAHQYQITGCCPLSPDCRLLATCUGGLKLWDTTRGQLAQFQHTYPSLNVCAP 1808
 Qy 787 FLNLEDPQEDMEVIVKCCWS-----ADGARIMVAAKRNKIFLPIHTSGLLGRIHTGH 839
 Db 1809 ----HPEGQ--VIATGWSWAGSISPFQVDGLKVTK-----DLGAPG----- 1842
 Qy 840 HSTIQYCDSPONHLAVVALSOYCQYELWNTDSRSKWDRCRGLSMYHGMFSPDGSSFLT 899
 Db 1843 -ASIRTIAENYGGIVYAVGRDLSMVLWREGARLAAPAHHGVAALFLHAGCQLLT 1901
 Qy 900 SDDDQTIRLW-----TKEVCKNSVMLKQEVDUTYFQENEVMVLAUDHTRRLQ 948
 Qy :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 1902 AGEDGKVQWGSGLSLGPGRGHGLSLSLSPALSVALSDGDRV-----AVGYRADGIRYKI 1956
 Qy 949 INGRGQDIDYEAQVSCCC-LSPHIIYAFGDENGAEITELL---VNNTRFQSRFH 1003
 Db 1957 SSGSQAQGOALDVAASALAMSP--KVLVSGAEDSLSQWTALKECSSLQSLWLSRFQ-- 2012
 Qy 1004 KTVWHQFTADEKTLISSDDEAIIQYWNWOL---DKC-1FLRGHOETV----- 1047
 Db 2013 KPV--LGATSQELLASADEFVQLMPQLTRPHKAEDPCGTLELRGIEGPVSCCSFS 2070
 Qy 1048 -----KDFRLL---KDFRLL-----KNSRLLSNSFDGTV 1067
 Db 2071 TDGGSLATGGRDRSLCWDRVTPKTPVLIHSFPACHRDWYTGCATWKDNELISCSDDGSV 2130
 Qy 1068 KWNIIITGNEKKEKDVFUVCHQGTW-----SCDI 1093
 Db 2131 GLWDPESGQRLGQFLGHOSAVASAVAAVEEHVSVSRDGTLLKWDHQGVELTSIPPASHGPI 2190
 Qy 1094 SHDATKXFSSTS-----DKTAKIWSFPLLPHELGHNCGYCRCSAFSVS 1139
 Db 2191 SHCAAAMEPRAQGQPSSELLVVTGQDGTRLWHPPLVQCQTHLGHSGPYRAAVSETS 2250
 Qy 1140 TLATGDDNGEIRKVNVSNGELLHLCAPLSEGAATHGGMVTDLQFSPDGMNLIS--AG 1196
 Db 2251 GLMLTAEDSGSVRLNQVPK-EADDTCIPRSEAA-----VTAWAAPDGSMAVSGNOAG 2302
 Qy 1197 GYIKWN---VVTGE-----SSQTFY 1214
 Db 2303 ELIIGQEAKAVATAQAPGHIGALIWSAHTFF 2334
 RESULT 10
 US-09-184-445-3
 ; Sequence 3 , Application US/09184445
 ; Parent No. 6174703
 ; GENERAL INFORMATION:
 ; APPLICANT: Harrington, Lea A.
 ; TITLE OF INVENTION: No. 6174703el Genes Encoding Telomerase Protein
 ; NUMBER OF INVENTION: 1
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: Amgen, Inc.
 ; STREET: 1840 De Havilland Drive
 ; CITY: Thousand Oaks
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 91320-1789
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0.0, Version #1.3.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/184,445
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/751,189
 ; FILING DATE: 15-NOV-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Oleksi, Nancy A.
 ; REGISTRATION NUMBER: 34,688
 ; REFERENCE/DOCKET NUMBER: A-433
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2627 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: unknown
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein
 US-09-184-445-3
 Query Match 6.2%: Score 408; DB 3; Length 2627;
 Best Local Similarity 21.0%; Pred. No. 4.1e-27;
 Matches 296; Conservative 170; Mismatches 492; Indels 454; Gaps 58;
 Qy 97 SSGKDSVSGITSYVVRTLCE-----GGPQRPRVVFVTRKLYNAIQQCLSK-- 142
 Db 1083 AAGRPYVGGLBEPGQLVQLQDQYWNM-QKLVYLQPGALEQ-PSPDDLYQATEQOLQKPP 1141
 Qy 143 -----LKBGPGWWTIHGNAGGGSVLAEARDHSLJEGCFPGSGS--- 182
 Db 1142 SPARRLQDVTQXLMPLPHGRSLSLT--GOSQGQKTAFLASLV--SALQ-A-PGAKYA 1194
 Qy 183 -----HWHSVKGKQDKSGLIMKLQNYCCTRLDQDESSSQLPLNIEAKDRLLRILMRKHPR 237
 Db 1195 XLVFFPHF-SGARPDDGSLALTLLRRLCTYLRQQLKEPGALPSTYRSLWELQQRLLPKSAE 1253

Db	1371	-----PLYLHVTDVLRFLTYEQYSERLRLTLPATPLIQLHSLTEQE-----	1415		2310 ELTNWQAKAVATAQAPGRVSHLIVYSANSFFVLSAN 2346
Qy	358	SYDYEALDMISVENFREDIKYTDTDSLTLQDKYKPTVKLCLIDMTEBEVDILEQE 417		RESULTS 112 US-09-060-836-4	
Db	1416	-HGHDVLQPAQT-ALETR-----SGLTVQDLHAIST---WILPKETKSWEVLA- 1462		; Sequence 4, Application US/09060836 ; Patent No. 581107	
Qy	418	FVNKSLLFCDRNG-----KSFRRYLHLDLQYDFLTKEKNSQQLDLHKKLIITOFQ 465		; GENERAL INFORMATION: ; APPLICANT: Harrington, Lea A. ; ADDRESS: Amgen, Inc.	
Db	1463	-----ASHSGNPFPLCPFAYLVGSLRSLLIGEGVERPAGRLCLSDGPRTTIXRRY 1514		; APPLICANT: Robinson, Murray O. ; TITLE OF INVENTION: No. 5981707el Genes Encoding Telomerase Protein	
Qy	466	R-----YHOPIHTLSPDQEDCMYTFN-----LAYHAMASAKMKELCA 502		; TITLE OF INVENTION: 1 ; NUMBER OF SEQUENCES: 12	
Db	1515	KRLGLEBLTAHVLLIAAHWKTCDPDASS-----TFRSCPPEAKLDLPHYLQSGNGLLAE 1569		; CORRESPONDENCE ADDRESS: ; STREET: 1840 De Havilland Drive	
Qy	503	LMFSLDWIKIKAKEVLYG-----PAHJH--HFVEYTHILDKDCAVSENFOEFLSANGHL 554		CITY: Thousand Oaks STATE: California	
Db	1570	PLTNLHYAATYLE-VGLVPDLLEAHVYASSKPEANQKLPAADV-----FHTFLRQASL 1625		COUNTRY: USA	
Qy	555	LGRQPFPNIVOLGLCPEBTSEYVQOAKLQAQEVNDGMYLEWINK---KNITNLUSRV 610		ZIP: 91320-1789	
Db	1626	LTCYPL-LLQOAAQSBEESPVCQCQPLTORWHD-QFTLKWINKPOTLKQQSLS-LT 1681		COMPUTER READABLE FORM:	
Qy	611	VRPHTDAYHACFSECGRIASCADKTLQVKAETGEK----- 649		MEDIUM TYPE: Floppy disk	
Db	1682	MSSSPPAV-----AFSPNGCORAAGVTASGTTIVLNLTQEBKAVVSGCDGSISSFAFSDTA 1738		COMPUTER: IBM PC compatible	
Qy	650	-----LIEKTAHEDEVLCACSTDFDIAETSVDRKVKTWNSMRTG 689		OPERATING SYSTEM: PC-DOS/MS-DOS	
Db	1739	LFLTTTPDGHLWLQHGWVFQTKHQAQYQITGCCUSPDRBLATVCGGYKLKDNTVRG 1798		SOFTWARE: Patentin Release #1.0, Version #1.30	
Qy	690	ELVHTYDEHSECVNCCHFTNSHHLLLATGSSDCDFKLKWLDNQKECRNTMFGHTNSVNHC 749		APPLICATION NUMBER: US 08/751,189	
Db	1799	QLAFOY-THPXSLNCAVAFHPEQG-----WATGWSAGSITFQDGLKTVKELGAPGSVCSL 1855		PRIORITY DATE: 08/15/1996	
Qy	750	RFSPPDDKLLACSAADGTKLMDATSANERKSINVKQ-----FRLNLED---POEME 798		ATTORNEY/AGENT INFORMATION:	
Db	1856	AFNKPCKSLVAVGRIDLSTVELWAWQEGARLAAPQCGCVSAYLFHLHAGRFLTAGED-- 1912		NAME: Oleksi, Nancy A.	
Qy	799	VIVKCCSWA----- 833		REGISTRATION NUMBER: 34,688	
Db	1913	-GKAQIWSGFGLPRPGCLSLPLSPALSVALNPQDQVAQGYREDGINIYKI-SSSQG 1969		REFERENCE/DOCKET NUMBER: A-433	
Qy	834	EIHTEGHSTIQCDFSPQNHIAVVALLSQYCVELWNTDSRSKVADCRGHLTSWHGUMFSPD 893		SEQUENCE CHARACTERISTICS:	
Db	1970	PQR-----QELNVAWSA-----VWLSPSVLVSQABDSL-----HGMIFKGD 2007		LENGTH: 2629 amino acids	
Qy	894	GSSFL-----TSDDQTIRLWETKVKCRNSAVMLQEVDVVFQE 932		TYPE: amino acid	
Db	2008	SLHSWLWLSRQKPVTLGAASRELMWAASESFVRLWPRQ----- 2047		STRANDEDNESS: unknown	
Qy	933	NEVMVIAVDHTRRLQI-----INGRTQDYLTEAGYSCCLSPHLYQTYA-----DENGAI 985		TOPOLOGY: unknown	
Db	2048	----LITQPHYHAVELPCCARLGH-----EGPVCCSFSPDGGILATAGRDRNLCC 2095		MOLECULE TYPE: protein	
Qy	986	EILELYNNRIFQSRFQ-HKCTYMHQFTADEKTLISSDDEAQWN-----WOLDKCIP 1039		US-09-060-836-4	
Db	2096	WDMKTAQPLIHTFSCHRDWTGCAWTD-NILVSCSSDGSVGLWNPAGQQLGQ----- 2151		Query Match Score 6.0% ; DB 2; Length 2629;	
Qy	1040	LRGHQETVKDPLKNSRLLWSFDCTVKNWITGNKEDFVCHGOTVLSCDISHDATAK 1099		Best Local Similarity 21.4%; Pred. No. 2.5e-26; Matches 290; Conservative 178; Mismatches 470; Indels 419; Gaps 62;	
Db	2152	FSGHQSAVASV-VAVEHIVSVSRDGTLYWD-----HQGVELTSIPAHSGPI 2198		QY 120 PORPYVFWTRKKLYNAIOOKLUSKLKGEPGMYTIGMAGCGK-----SVLAABAVRDHSLL 174	
Qy	1100	FSSTSAA-----DRTKIAWSFPLLPPLPHELGNGCVRCSAFVSVD 1139		Db 1152 PARP-----RLLQDVTQOLLPGRLSLMT--QAGQGRTAFAFLASLVSALKVPPQ--- 1199	
Qy	2199	SQCAALEPRPGCOPSEELLVVTGFLDGTAKLWHPILCVQIRTLOCHSGPTAAASEAS 2258		QY 175 EGCPFGCGVHFTV---SVGKDPDKSGLMKLNQLCFDQESFSQLPQPLNIEAKBLRL 230	
Db	1140	TLLATGPDNGEGRINWVNGELLHLCAPLSEEGRATHGMMWYTDLCSFDGKMLISA-GG 1197		Db 1200 ---PNEPPPFVFFHAAARDQCLAZLNLRLRKLGELSPSTYRGLYMELQQK 1255	
Qy	2259	GLLLTSDDS-SVQLWQPK-BADDSTPKRSSVA-----ITAVAWADPSGMVVGNEAG 2309		QY 231 MLRKHPSL-----LILD-----DWWDWVFLKAFDSQQFLNQMLLAKQSSL- 1370	
Db	1198	YIKWN-----VVTGE-----SSQTFYTINGTN 1219		Db 1256 LLLKPAQSLOPAQTIVLIIINGADKLYVDRNGQOLISWPKSLPRTVHLVLSVS---SDSG 1311	
Qy		:	:	QY 274 MGP-----KYYVPEVSSLGKRG---LEILSL-----FVNMKKADLPQEAHSII 314	
		:	:	Db 1312 IGETLQSQSAYWVAGLSSVSSRAQLVREBELAYGKRLEBSPFNMQMRILLAKQSSL- 1370	
		:	:	QY 315 KECKGSPVLSLIGHLLRDF-----PNRWEYKLKOLQNQFKRIRKSS 357	
		:	:	Db 1371 ----PLVLYLHTVYLRLFTLYEQYSERLRTLPLPLQHQLSTLQE----- 1415	
		:	:	QY 358 SYDVALDEAMPSYMLREDIKYDVTDSLILQKVVKPFLKVLCLWDMTEEVSDILQ 417	
		:	:	Db 1416 -HGHDVLPQALT-ALEVTR-----SGLTVQLEHAILST--WILPKETKSMEVLA- 1462	

GENERAL INFORMATION:

APPLICANT: Harrington, Lea A.

INVENTOR: Robinson, Murray C.

TITLE OF INVENTION: No. 6174703el Genes Encoding Telomerase Protein

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Amgen, Inc.

STREET: 1840 De Havilland Drive

CITY: Thousand Oaks

STATE: California

ZIP: 91320-1789

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/184,445

FILING DATE: US/09/184,445

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/751,189

FILING DATE: 15-NOV-1996

ATTORNEY/AGENT INFORMATION:

NAME: Oleksi, Nancy A.

REGISTRATION NUMBER: 34,688

REFERENCE/DOCKET NUMBER: A-433

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 2629 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-09-184-445-4

Qy 418 FVNKSLLFCDRNG-----KSPRYLHDLOQDFTERNCSQOLDLHKKJITQFQ 465

Db 1463 -----ASHSGNPPPLCPFAYLQYQSLRSLGEGPVERPARCLSDGLPRTTICKRYG 1514

Qy 466 R-----YHOPHTLSPDQEDCMWYNP-----LAYHMASAKMHHKELCA 502

Db 1515 KRIGLEKTAHVLLAHLWKCDPDAHG----TRFSCPEALDKDLYHLLQSNHGLAE 1569

Qy 503 LMPSLDVTKAETKELVG----PAHLTH-SEVEYRHILDEKDCASENFORPELSNLGH 554

Db 1570 FLTNLHVAYALE-YCLVPLDLHEAHVLVASSKPEANQKLPAADIV--FHTFLRQASL 1625

Qy 555 LGQQPFNPVIVQGLCSPETBEVYQAKLQAKQDVDMGLTYLEWINK---KNTNLSRLV 610

Db 1626 LTQYPL-LLQQAASPEEPVCCOAPLTQWHD-QFTLKVWKPKTLKGQSLS-LT 1681

Qy 611 VRPHTDAYVHACSFEDGORASACADKTQLQVKFAETGEK----- 649

Db 1682 MSSPTAV----AFSPNGORAVGATSGTYIUNLKWOERKAVVSGCDGISSPAFLSDTA 1738

Qy 650 -----LLETKAHEDEVLCATFCAFSSTDPRFIATCSVDKKYKVINNSMTG 689

Db 1739 LFLLTFDGHLELWDLQHGMVFQTKAHQYQITGCCSPDRRLATVCGYKLWDIVRG 1798

Qy 690 ELVHTYDEHSECVNCCHFTNSHILLATGSDCFKLWLNOKECRATMFMCHTNTSYHNC 749

Db 1799 QLAFOY-THPSLNCYAFHPEQG-VVATGSNAGSITPFDAGLKVTKELGARGPSVCSL 1855

Qy 750 RFSPDDKLASSADDTKLWUDATSAKRSANSRKSVNKQ-----POIDMB 798

Db 1856 AFNPKPGKIVAVGRIDGTVELW-AWQEGARLAFFPAQCGCVSAVLFHAGDRFTAGED-- 1912

Qy 799 VIVKCCWSA-----DGARIMVA-AKNNKFLFLDHTSLLG 33

Db 1913 --GRAQIWSGFGRPGCLGSLPLSPALSVLPNDGQDVAQGYREDGINYKCI-SSSQG 1969

Qy 834 EHTGHHSTIQYCDFSQNHLAVVALLSQYCWLWNTDSRSKVA'DCRGHLSTMVGMFSPD 893

Db 1970 PQH-----QELNAYASL-----TSSDODTRIWEKVCNSAVMLKQEVDVVFQE 932

Qy 894 GSSFL-----SLISLWILSRYOKPVIGLASRELMAASEDFVRLWPRO----- 2047

Db 2008 SLISLWILSRYOKPVIGLASRELMAASEDFVRLWPRO----- 2047

Qy 933 NEVNLAVDHARRLQI----INGRTQDYLITEAOVSCCOLSPHLOVIAGF-DENGAI 985

Db 2048 ---LTTQPHYHAVELPCCELRH-----EGVCCCSFSDGGITLATAGRDRNLIC 2095

Qy 986 EILEFLDNNTFOSRFQ-HKKTWHIQFTADEFKLJSSDAAELOWN--WOLDKCIF 1039

Db 2096 WDNIKIAQAPLILHTHFTSSCHDWITGCAVTKD-NILVSCSSPSGVSGLWNEPAGSGLGQ--- 2151

Qy 1040 LRHQETVYKDPFLKNSRULSWSFDGTVKVNWNITENKEKFVCHQGTVLSCDISHDATAK 1099

Db 2125 PFGHQSAVSAV-VAVEEHISUVRSDGTLKWD-----HOGVELTSPANSGPI 2198

Qy 1100 FSSTSA-----DXTAKIWSFDLPLHIEQRGNGCVRCSAFSVDS 1139

Db 2199 SQCAAALERPGQQGPGSELVUVTVGLDGATKLWPHLUVQIRTLQGHSGPVTAASEAS 2258

Qy 1140 TLIATGDGNGETRIWVNSCELLCAPLSSEGATHGGWWTDLCPSPGKMLISA-GG 1197

Db 2259 GLLTSDDS-SVQLQIPK-EADDSYKERSYSA-----ITAVAWPDGSIVVSGENEAG 2309

Qy 1198 YIKWN-----YVTGE-----SSQTFTYNTGN 1219

Db 2310 ELTLWQOQAVATAQPRVSHLTWSANSFFVLSAN 2346

RESULT 13

US-09-184-445-4

Sequence 4, Application US/09184445

Patent No. 6174703

Qy 674 TCSYDKRKVTKWNSMTGELVITYDEHSBQNCCHFTNSSHILLATGSSPCFLWLWDINQK 733
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 72 SGEDGTPARLWN----- -VATGTEHAVIK----- 94
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Qy 734 ECRNTMFGHTNSVNHCRESDDKKLASCADSTKLKDATSANERKSINVQFFNLNEDP 793
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 95 -----GHITDYYAVAFSDGSNAVASSRDRGTRWVATGKERDV-----LQAP 138
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Qy 794 QEDMEVIVKCCSWADGARIMVAAKNKFLEDFIHTSGLGE-IHT-GHHSIQCDFSP 850
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 139 AEN---VSLSLAFSPDGSMNHGDSTVHLWDVAS---GEALITFEGHTDWRAVAFSP 190
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Qy 851 QNHLLAVVALLSQYCVELWNTDSRSKVADCRGLHSWIGVMFSPDGSSFLTSSDDQTIRLW 909
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 191 DGALLASGSDRTIRLWDVAQBEHTILEGHTEPVHSVAFPEGTTLASASDGTRIW 249
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

Search completed: January 27, 2005, 18:41:52
 Job time : 35 secs